GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: July 9, 2005, 13:18:09 ; Search time 19 Seconds
(without alignments)
2992.848 Million cell updates/sec

Title: US-10-659-549-3
Perfect score: 3043
Sequence: 1 MALEIHMSDPMCLIENFNEQ.....GEAARSCGSQQGVWSQKVWV 591

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1958.5	64.4	592	2	A41268	guanine nucleotide
2	1897	62.3	591	2	S70524	guanine nucleotide
3	1765.5	58.0	589	2	A46459	macrophage-activat
4	1757.5	57.8	591	2	S43506	hypothetical prote
5	1365.5	44.9	623	2	I49684	guanylate binding
6	251.5	8.3	555	2	T17320	hypothetical prote
7	216	7.1	217	2	A84810	probable guanylate
8	213.5	7.0	991	2	H86168	hypothetical prote
9	171.5	5.6	4574	2	G02520	plectin - human
10	171.5	5.6	4684	2	A59404	plectin [imported]
11	160.5	5.3	1291	2	T22382	hypothetical prote
12	160.5	5.3	1690	2	T13030	microtubule bindin
13	160.5	5.3	4687	1	A39638	plectin - rat
14	159.5	5.2	862	2	T49593	hypothetical prote
15	158	5.2	464	2	H90279	microtubule bindin
16	156.5	5.1	1410	1	A57013	early endosome ant
17	155.5	5.1	762	2	T50155	hypothetical prote
18	154.5	5.1	853	2	T23697	hypothetical prote
19	154.5	5.1	1392	2	A43336	microtubule-vesicl
20	154.5	5.1	1427	2	S22695	restin - human
21	153	5.0	944	2	S26710	spindle pole body
22	151.5	5.0	992	2	T46337	hypothetical prote
23	151	5.0	1290	2	A55094	chromosomal protei
24	151	5.0	1818	1	S73852	hypothetical prote
25	148	4.9	577	1	S39804	moesin - pig
26	148	4.9	1288	2	T46486	chromosomal protei
27	147.5	4.8	429	2	S29565	apolipoprotein A-I
28	147.5	4.8	1790	2	S67593	transport protein
29	147	4.8	407	2	S23325	M2 protein precurs
30	146	4.8	586	1	B41129	ezrin - mouse
31	146	4.8	742	2	S56337	hypothetical prote
32	146	4.8	925	2	T01384	hypothetical prote
33	145.5	4.8	1426	2	T00337	hypothetical prote
34	145	4.8	742	2	C91265	probable vimentin
35	145	4.8	742	2	H86105	probable vimentin
36	145	4.8	1178	2	S78475	mannosylphosphoryl
37	144	4.7	871	2	D86355	protein T16E15.12
38	144	4.7	980	2	E71606	hypothetical prote
39	143.5	4.7	864	2	B90395	purine NTPase (imp
40	143.5	4.7	1875	2	S38173	myosin-like protei
41	143.5	4.7	1992	2	A47297	myosin heavy chain
42	142.5	4.7	1164	2	T24806	hypothetical prote
43	142.5	4.7	2442	2	T08621	centrosome associa
44	142	4.7	657	2	S05517	lamin - chicken
45	142	4.7	1972	1	A41604	myosin heavy chain

ALIGNMENTS

RESULT 1
A41268
guanine nucleotide-binding protein 1 - human
C;Species: Homo sapiens (man)
C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 09-Jul-2004
C;Accession: A41268
R;Cheng, Y.S.E.; Patterson, C.E.; Staeheli, P.
Mol. Cell. Biol. 11, 4717-4725, 1991
A;Title: Interferon-induced guanylate-binding proteins lack an N(T)KXD consensus motif
A;Reference number: A41268; MUID:91342675; PMID:1715024
A;Accession: A41268
A;Molecule type: mRNA
A;Residues: 1-592 <CHE>
A;Cross-references: UNIPROT:P32455; GB:M55542; NID:g183001; PIDN:AAA35871.1; PID:g18300
C;Genetics:
A;Gene: GDB:GBP1
A;Cross-references: GDB:378351; OMIM:600411
A;Map position: 1pter-1qter
C;Superfamily: guanine nucleotide-binding protein 1

Query Match 64.4%; Score 1958.5; DB 2; Length 592;
Best Local Similarity 69.4%; Pred. No. 7.6e-101;
Matches 387; Conservative 71; Mismatches 89; Indels 11; Gaps 3;

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Qy          1 MALEIHMSDPMCLIENFNEQLKVNQEALEILSAITQPVVVVAIVGLYRTGKSYLMNKLAG 60
              || ||||: ||||||| | :|  | |||:||||||||:||||||||||||||||||||||
Db          1 MASEIHMTGPMCLIENTNGRLMANPEALKILSAITQPMVVVAIVGLYRTGKSYLMNKLAG 60

Qy         61 KNKGFSVASTVQSHTKGIWIWCVPHPNWPNHTLVLLDTEGLGDVEKADNKNDIQIFALAL 120
              | ||||: ||||||||||||:||||||  | | |||||||||||||| ||:||  |||||:
Db         61 KKKGFSLGSTVQSHTKGIWMWCVPHPKKPGHILVLLDTEGLGDVEKGDNQNDSWIFALAV 120

Qy        121 LLSSTFVYNTVNKIDQGAIDLLHNVTELTDLLKARNSPD--LDRVEDPADSASFFPDLVW 178
              |||||||||::  |:| |:| |: |||||  :::::|||   : ||| ||  ||||| ||
Db        121 LLSSTFVYNSIGTINQQAMDQLYYVTELTHRIRSKSSPDENENEVEDSADFVSFFPDFVW 180

Qy        179 TLRDFCLGLEIDGQLVTPDEYLENSLRPKQGSDQRVQNFNLPRLCIQKFFPKKKCFIFDL 238
              |||||  | || ||| :|||||  ||: |:|: |: : ||||||||:|||||||||:||
Db        181 TLRDFSLDLEADGQPLTPDEYLTYSLKLKKGTSQKDETFNLPRLCIRKFFPKKKCFVFDR 240

Qy        239 PAHQKKLAQLETLPDDELEPEFVQQVTEFCSYIFSHSMTKTLPGGIMVNGSRLKNLVLTY 298
              | |::|||||| | |:||:|||||| :|||||||:| |||| ||| ||| ||::|||||
Db        241 PVHRRKLAQLEKLQDEELDPEFVQQVADFCSYIFSNSKTKTLSGGIQVNGPRLESLVLTY 300

Qy        299 VNAISSGDLPCIENAVLALAQRENSAAVQKAIAHYDQQMGQKVQLPMETLQELLDLHRTS 358
              |||||||||||:|||||||| ||||||||||||:|||||||||| |:|||||||| |
Db        301 VNAISSGDLPCMENAVLALAQIENSAAVQKAIAHYEQQMGQKVQLPTESLQELLDLHRDS 360

Qy        359 EREAIEVFMKNSFKDVDQSFQKELETLLDAKQNDICKRNLEASSDYCSALLKDIFGPLEE 418
              |||||||:::|||||  |||||   |: |::| ||:| ||||| || ||: || ||||
Db        361 EREAIEVFIRSSFKDVDHLFQKELAAQLEKKRDDFCKQNQEASSDRCSGLLQVIFSPLEE 420
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Qy        419 AVKQGIYSKPGGHNLFIQKTEELKAKYYREPRKGIQAEEVLQKYLKSKESVSHAILQTDQ 478
Db        421 EVKAGIYSKPGGYRLFVQKLQDLKKKYYEEPRKGIQAEEILQTYLKSKESMTDAILQTDQ 480

Qy        479 ALTETEKKKKEAQVKAEAEKAEAQRLAAIQRQNEQMMQERERLHQEQVRQ----MEIAKQ 534
Db        481 TLTEKEKEIEVERVKAESAQASAKMLQEMQRKNEQMMEQKERSYQEHLKQLTEKMENDRV 540

Qy        535 NWLAEQQ-----KMQEQQ 547
Db        541 QLLKEQERTLALKLQEQE 558
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RESULT 2
S70524
guanine nucleotide-binding protein 2 - human
C;Species: Homo sapiens (man)
C;Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004
C;Accession: S70524; S70523; B41268
R;Schwemmle, M.
submitted to the EMBL Data Library, May 1995
A;Reference number: S70524
A;Accession: S70524
A;Molecule type: mRNA
A;Residues: 1-591 <SCH>
A;Cross-references: UNIPROT:P32456; EMBL:M55543; NID:g829176; PIDN:AAA67323.1; PID:g8291
R;Neun, R.; Richter, M.F.; Staeheli, P.; Schwemmle, M.
FEBS Lett. 390, 69-72, 1996
A;Title: GTPase properties of the interferon-induced human guanylate-binding protein 2.
A;Reference number: S70523; MUID:96314551; PMID:8706832
A;Accession: S70523
A;Molecule type: mRNA
A;Residues: 1-19 <NEU>
A;Cross-references: EMBL:M55543
R;Cheng, Y.S.E.; Patterson, C.E.; Staeheli, P.
Mol. Cell. Biol. 11, 4717-4725, 1991
A;Title: Interferon-induced guanylate-binding proteins lack an N(T)KXD consensus motif a
A;Reference number: A41268; MUID:91342675; PMID:1715024
A;Accession: B41268
A;Molecule type: mRNA
A;Residues: 'Q',7,'A',9-10,'NEP',14-591 <CHE>
A;Cross-references: GB:M55543
C;Genetics:
A;Gene: GDB:GBP2
A;Cross-references: GDB:378363
C;Superfamily: guanine nucleotide-binding protein 1

  Query Match   62.3%; Score 1897; DB 2; Length 591;
  Best Local Similarity 63.5%; Pred. No. 1.9e-97;
  Matches 377; Conservative   88; Mismatches 101; Indels   28; Gaps   4;

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Qy          1 MALEIHMSDPMCLIENFNEQLKVNQEALEILSAITQPVVVVAIVGLYRTGKSYLMNKLAG 60
Db          1 MAPEINLPGPMSLIDNTKGQLVVNPEALKILSAITQPVVVVAIVGLYRTGKSYLMNKLAG 60

Qy         61 KNKGFSVASTVQSHTKGIWIWCVPHPNWPNHTLVLLDTEGLGDVEKADNKNDIQIFALAL 120
Db         61 KKNGFSLGSTVKSHTKGIWMWCVPHPKKPEHTLVLLDTEGLGDIEKGDNENDSWIFALAI 120

Qy        121 LLSSTFVYNTVNKIDQGAIDLLHNVTELTDLLKARNSPDLDRVEDPADSASFFPDLVWTL 180
Db        121 LLSSTFVYNSMGTINQQAMDQLHYVTELTDRIKANSSPGNNSVDDSADFVSFFPAFVWTL 180

Qy        181 RDFCLGLEIDGQLVTPDEYLENSLRPKQGSDQRVQNFNLPRLCIQKFFPKKKCFIFDLPA 240
Db        181 RDFTLELEVDGEPITADDYLELSLKLRKGTDKKSKSFNDPRLCIRKFFPKRKCFVFDWPA 240

Qy        241 HQKKLAQLETLPDDELEPEFVQQVTEFCSYIFSHSMTKTLPGGIMVNGSRLKNLVLTYVN 300
Db        241 PKKYLAHLEQLKEEELNPDFIEQVAEFCSYILSHSNVKTLSGGIAVNGPRLESLVLTYVN 300

Qy        301 AISSGDLPCIENAVLALAQRENSAAVQKAIAHYDQQMGQKVQLPMETLQELLDLHRTSER 360
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Db        301 AISSGDLPCMENAVLALAQIENSAAVEKAIAHYEQQMGQKVQLPTETLQELLDLHRDSER 360

Qy        361 EAIEVFMKNSFKDVDQSFQKELETLLDAKQNDICKRNLEASSDYCSALLKDIFGPLEEAV 420
Db        361 EAIEVFMKNSFKDVDQMFQRKLGAQLEARRDDFCKQNSKASSDCCMALLQDIFGPLEEDV 420

Qy        421 KQGIYSKPGGHNLFIQKTEELKAKYYREPRKGIQAEEVLQKYLKSKESVSHAILQTDQAL 480
Db        421 KQGTFSKPGGYRLFTQKLQELKNKYYQVPRKGIQAKEVLKKYLESKEDVADALLQTDQSL 480

Qy        481 TETEKKKKEAQVKAEAEKAEAQRLAAIQRQNEQMMQERERLHQEQVRQ----MEIAKQNW 536
Db        481 SEKEKAIEVERIKAESAEAAKKMLEEIQKKNEEMMEQKEKSYQEHVKQLTEKMERDRAQL 540

Qy        537 LAEQQ-----KMQEQQMQVFINCFISPLPVTMRVCSSGKEGEAARSCGSQQGVW 585
Db        541 MAEQEKTLALKLQEQE----------------RLLKEGFENESKR---LQKDIW 575
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RESULT 3
A46459
macrophage-activation gene-1 protein mag-1 - mouse
N;Alternate names: guanine nucleotide-binding protein 1; interferon-gamma inducible prot
C;Species: Mus musculus (house mouse)
C;Date: 18-Jun-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C;Accession: A46459; C41268
R;Wynn, T.A.; Nicolet, C.M.; Paulnock, D.M.
J. Immunol. 147, 4384-4392, 1991
A;Title: Identification and characterization of a new gene family induced during macroph
A;Reference number: A46459; MUID:92091752; PMID:1753106
A;Accession: A46459
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-589 <WYN>
A;Cross-references: UNIPROT:Q01514; GB:M63961; NID:g198999; PIDN:AAA39486.1; PID:g199000
A;Experimental source: RAW 264.7 macrophage cell line
A;Note: sequence extracted from NCBI backbone (NCBIP:72196)
R;Cheng, Y.S.E.; Patterson, C.E.; Staeheli, P.
Mol. Cell. Biol. 11, 4717-4725, 1991
A;Title: Interferon-induced guanylate-binding proteins lack an N(T)KXD consensus motif a
A;Reference number: A41268; MUID:91342675; PMID:1715024
A;Accession: C41268
A;Molecule type: mRNA
A;Residues: 1-589 <CHE>
A;Cross-references: GB:M55544; NID:g193439; PIDN:AAA37666.1; PID:g193440
C;Genetics:
A;Gene: MAG-1
C;Superfamily: guanine nucleotide-binding protein 1

  Query Match   58.0%; Score 1765.5; DB 2; Length 589;
  Best Local Similarity 61.7%; Pred. No. 3.4e-90;
  Matches 343; Conservative   95; Mismatches 109; Indels   9; Gaps   2;

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Qy          1 MALEIHMSDPMCLIENFNEQLKVNQEALEILSAITQPVVVVAIVGLYRTGKSYLMNKLAG 60
Db          1 MASEIHMSEPMCLIENTEAQLVINQEALRILSAITQPVVVVAIVGLYRTGKSYLMNKLAG 60

Qy         61 KNKGFSVASTVQSHTKGIWIWCVPHPNWPNHTLVLLDTEGLGDVEKADNKNDIQIFALAL 120
Db         61 KRTGFSLGSTVQSHTKGIWMWCVPHPKKAGQTLVLLDTEGLEDVEKGDNQNDCWIFALAV 120

Qy        121 LLSSTFVYNTVNKIDQGAIDLLHNVTELTDLLKARNSPDLDRVEDPADSASFFPDLVWTL 180
Db        121 LLSSTFIYNSIGTINQQAMDQLHYVTELTDLIKSKSSPDQSDVDNSANFVGFFPIFVWTL 180

Qy        181 RDFCLGLEIDGQLVTPDEYLENSLRPKQGSDQRVQNFNLPRLCIQKFFPKKKCFIFDLPA 240
Db        181 RDFSLDLEFDGESITPDEYLETSLALRKGTDENTKKFNMPRLCIRKFFPKRKCFIFDRPG 240

Qy        241 HQKKLAQLETLPDDELEPEFVQQVTEFCSYIFSHSMTKTLPGGIMVNGSRLKNLVLTYVN 300
Db        241 DRKQLSKLEWIQEDQLNKEFVEQVAEFTSYIFSYSGVKTLSGGITVNGPRLKSLVQTYVS 300
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Qy        301 AISSGDLPCIENAVLALAQRENSAAVQKAIAHYDQQMGQKVQLPMETLQELLDLHRTSER 360
Db        301 AICSGELPCMENAVLTLAQIENSAAVQKAITYYEEQMNQKIHMPTETLQELLDLHRTCER 360

Qy        361 EAIEVFMKNSFKDVDQSFQKELETLLDAKQNDICKRNLEASSDYCSALLKDIFGPLEEAV 420
Db        361 EAIEVFMKNSFKDVDQKFQEELGAQLEAKRDAFVKKNMDMSSAHCSDLLEGLFAHLEEEV 420

Qy        421 KQGIYSKPGGHNLFIQKTEELKAKYYREPRKGIQAEEVLQKYLKSKESVSHAILQTDQAL 480
Db        421 KQGTFYKPGGYYLFLQRKQELEKKYIQTPGKGLQAEVMLRKYFESKEDLADTLLKMDQSL 480

Qy        481 TETEKKKKEAQVKAEAEKAEAQRLAAIQRQNEQMMQERERLHQEQVRQ----MEIAKQNW 536
Db        481 TEKEKQIEMERIKAEAAEAANRALAEMQKKHEMLMEQKEQSYQEHMKQLTEKMEQERKEL 540

Qy        537 LAEQQ-----KMQEQQ 547
Db        541 MAEQQRIISLKLQEQE 556


RESULT 4
S43506
hypothetical protein - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
C;Accession: S43506
R;Asundi, V.K.; Stahl, R.C.; Showalter, L.; Conner, K.J.; Carey, D.J.
Biochim. Biophys. Acta 1217, 257-265, 1994
A;Title: Molecular cloning and characterization of an isoprenylated 67 kDa protein.
A;Reference number: S43506; MUID:94198287; PMID:8148370
A;Accession: S43506
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-591 <ASU>
A;Cross-references: UNIPROT:Q63663; EMBL:M80367; NID:g207604; PIDN:AAA19909.1; PID:g2076
C;Superfamily: guanine nucleotide-binding protein 1

  Query Match             57.8%;  Score 1757.5;  DB 2;  Length 591;
  Best Local Similarity   63.3%;  Pred. No. 9.5e-90;
  Matches  346;  Conservative   82;  Mismatches  116;  Indels    3;  Gaps    1;

Qy          1 MALEIHMSDPMCLIENFNEQLKVNQEALEILSAITQPVVVVAIVGLYRTGKSYLMNKLAG 60
Db          3 MASEIHMLQPMCLIENTEAHLVINQEALRILSAINQPVVVVAIVGLYRTGKSYLMNKLAG 62

Qy         61 KNKGFSVASTVQSHTKGIWIWCVPHPNWPNHTLVLLDTEGLGDVEKADNKNDIQIFALAL 120
Db         63 KRTGFSLGSTVQSHTKGIWMWCVPHPKKAGQTLVLLDTEGLEDVEKGDNQNDCWIFALAV 122

Qy        121 LLSSTFVYNTVNKIDQGAIDLLHNVTELTDLLKARNSPDLDRVEDPADSASFFPDLVWTL 180
Db        123 LLSSTFVYNSMGTINQQAMDQLHYVTELTDLIKSKSSPDQSGIDDSANFVGFFPTFVWAL 182

Qy        181 RDFCLGLEIDGQLVTPDEYLENSLRPKQGSDQRVQNFNLPRLCIQKFFPKKKCFIFDLPA 240
Db        183 RDFSLELEVNGKLVTPDEYLEHSLTLKKGADKKTKSFNEPRLCIRKFFPKRKCFIFDRPA 242

Qy        241 HQKKLAQLETLPDDELEPEFVQQVTEFCSYIFSHSMTKTLPGGIMVNGSRLKNLVLTYVN 300
Db        243 LRKQLCKLETLGEEELCSEFVEQVAEFTSYIFSYSAVKTLSGGIIVNGPRLKSLVQTYVG 302

Qy        301 AISSGDLPCIENAVLALAQRENSAAVQKAIAHYDQQMGQKVQLPMETLQELLDLHRTSER 360
Db        303 AISSGSLPCMESAVLTLAQIENSAAVQKAITHYEEQMNQKIQMPTETLQELLDLHRLIER 362

Qy        361 EAIEVFMKNSFKDVDQSFQKELETLLDAKQNDICKRNLEASSDYCSALLKDIFGPLEEAV 420
Db        363 EAIEIFLKNSFKDVDQKFQTELGNLLISKRDAFIKKNSDVSSAHCSDLIEDIFGPLEEEV 422

Qy        421 KQGIYSKPGGHNLFIQKTEELKAKYYREPRKGIQAEEVLQKYLKSKESVSHAILQTDQAL 480
Db        423 KQGTFSKPGGYFLFLQMRQELEKKYNQAPGKGLEAEAVLKKYFESKEDIVETLLKTDQSL 482

Qy        481 TETEKKKKEAQVKAEAEKAEAQRLAAIQRQNEQMMQERERLHQEQVRQMEIAKQNWLAEQ 540
Db        483 TEAAKEIEVERIKAETAEAANRELAEKQEKFELMMQQKEESYQEHVRQL---TEKMKEEQ 539

Qy        541 QKMQEQQ 547
Db        540 KKLIEEQ 546


RESULT 5
I49684
guanylate binding protein - mouse
C;Species: Mus musculus (house mouse)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C;Accession: I49684
R;Wynn, T.A.; Nicolet, C.M.; Paulnock, D.M.
J. Immunol. 147, 4384-4392, 1991
A;Title: Identification and characterization of a new gene family induced during macroph
A;Reference number: A46459; MUID:92091752; PMID:1753106
A;Accession: I49684
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-623 <RES>
A;Cross-references: UNIPROT:Q61594; GB:M81128; NID:g193443; PIDN:AAA37668.1; PID:g19344
C;Superfamily: guanine nucleotide-binding protein 1

  Query Match             44.9%;  Score 1365.5;  DB 2;  Length 623;
  Best Local Similarity   49.3%;  Pred. No. 4.5e-68;
  Matches  267;  Conservative  112;  Mismatches  150;  Indels   13;  Gaps    3;

Qy         10 PMCLIENFNEQLKVNQEALEILSAITQPVVVVAIVGLYRTGKSYLMNKLAGKNKGFSVAS 69
Db          8 PICLVENHNEQLSVNQEAIEILDKISQPVVVVAIVGWSHTGKSYLMNCLAGQNHVFPLGS 67

Qy         70 TVQSHTKGIWIWCVPHPNWPNHTLVLLDTEGLGDVEKADNKNDIQIFALALLLSSTFVYN 129
Db         68 TVQSQTKGIWMWCMPHPTKPEHTLVLLDTEGLGDVEKGDPKNDLWIFALSVLLSSTFVYN 127

Qy        130 TVNKIDQGAIDLLHNVTELTDLLKARNSPDLDRVEDPADSASFFPDLVWTLRDFCLGLEI 189
Db        128 SMNTINHQALEQLHYVTELTELIRAKSSPNPHGIKNSTEFVSFFPDFVWTVRDFMLELKL 187

Qy        190 DGQLVTPDEYLENSLRPKQGSDQRVQNFNLPRLCIQKFFPKKKCFIFDLPAHQKKL-AQL 248
Db        188 NGEDITSDEYLENALKLIPGNNPRIQASNSARECIRRFFPNRKCFVFEWPTHDIELIKQL 247

Qy        249 ETLPDDELEPEFVQQVTEFCSYIFSHSMTKTLPGGIMVNGSRLKNLVLTYVNAISSGDLP 308
Db        248 ETISEDQLDPTFKESAMAFASYIFTYAKIKTLREGIKVTGNGLGTLVTTYVDAINSGAVP 307

Qy        309 CIENAVLALAQRENSAAVQKAIAHYDQQMGQKVQLPMETLQELLDLHRTSEREAIEVFMK 368
Db        308 CLDDAVTTLAQRENSVAVQKAASHYSEQMAQRLSLPTDTIQELLDVHAACEKEAMAVFME 367

Qy        369 NSFKDVDQSFQKELETLLDAKQNDICKRNLEASSDYCSALLKDIFGPLEEAVKQGIYSKP 428
Db        368 HSFKDENQQFLKKLVELLREKNGLFLLKNEEASDKYCQEELDRLSKDLMDNI--STFSVP 425

Qy        429 GGHNLFIQKTEELKAKYYREPRKGIQAEEVLQKYLKSKESVSHAILQTDQALTETEKKKK 488
Db        426 GGHRLYMDMREKIEHDYWQVPRKGVKASEVFQNFLQSQAIIESSILQADTALTAGQKAIA 485

Qy        489 EAQVKAEAEKAEAQRLAAIQRQNEQMMQERERLHQEQVRQMEIAKQNWLAEQQKMQEQQM 548
Db        486 EKHTKKEAAEKEQDLLRQKQKEHQEYMEAQEKRNKENLEQL----------RRKLEQERE 535

Qy        549 QV 550
Db        536 QL 537


RESULT 6
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```
T17320
hypothetical protein DKFZp564J0863.1 - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T17320
R;Duesterhoeft, A.; Lauber, J.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.
submitted to the Protein Sequence Database, September 1999
A;Reference number: Z18727
A;Accession: T17320
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-555 <DUE>
A;Cross-references: UNIPROT:Q9UFL1; EMBL:AL117600
A;Experimental source: fetal brain; clone DKFZp564J0863
C;Genetics:
A;Note: DKFZp564J0863.1

  Query Match             8.3%;  Score 251.5;  DB 2;  Length 555;
  Best Local Similarity   24.9%;  Pred. No. 1.2e-06;
  Matches  112;  Conservative   68;  Mismatches  182;  Indels   87;  Gaps   19;

Qy          2 ALEIHMSDP--MCLIENFNEQLKVNQEALEILSAITQ------PVVVVAIVGLYRTGKSY 53
              |:|     |  : |::      :::::||   | : |       ||||:: | :| |||:
Db         32 AMESSKPGPVQVVLVQKDQHSFELDEKAL--ASILLQDHIRDLDVVVVSVAGAFRKGKSF 89

Qy         54 LMN---------KLAGKNK----------GFSVASTVQSHTKGIWIW----CVPHPNWPN 90
              :::         | :| :          |||       | || ||     |  |
Db         90 ILDFMLRYLYSQKESGHSNWLGDPEEPLTGFSWRGGSDPETTGIQIWSEVFTVEKPGGKK 149

Qy         91 HTLVLLDTEGLGDVEKADNKNDIQIFALALLLSSTFVYNTVNKIDQGAIDLLHNVTELTD 150
                :||:||:|  |  ::  |:   ||||: : ||  :||    | :  :  |   ||
Db        150 VAVVLMDTQGAFD-SQSTVKDCAAIFALSTMTSSVQIYNLSQNIQEDDLQQLQLFTEYGR 208

Qy        151 LLKARNSPDLDRV-EDPADSASFFPDLVWTLRDFCLGLEIDGQLVTPDEYLENSLRPKQG 209
              |         :| :   |       |  |:: :||     |     |     :|:  |: |:
Db        209 LA-------MDEIFRKP------FQTLMFLVRDRSFPYEYSYGLQGGMAFLDKRLQVKEH 255

Qy        210 SDQRVQNFNLPRLCIQKFFPKKKCFIFDLPAHQKKLAQLETLPD-----DELEPEFVQQV 264
              : :||    |  |   |    ||:   |        |: | ||      ::  || :|:
Db        256 QHEEIQNV---RNHIHSCFSDVTCFLLPHPG-----LQVATSPDFDGKLKDIAGEFKEQL 307

Qy        265 TEFCSYIFSHSMTKTLPGGIM---VNGSR-----LKNLVLTYVNAISSGDLPCIENAVLA 316
                  |: :       |  :|   :|||:     |       |:      |||  :: : |
Db        308 QALIPYVLN-------PSKLMEKEINGSKVTCRGLLEYFKAYIKIYQGEDLPHPKSMLQA 360

Qy        317 LAQRENSAAVQKAIAHYDQQM-----GQKVQLPMETLQELLDLHRTSEREAIEVFMKN-- 369
              |:  | ||    |   |   |      |:|  |  : |:|    |   :: |:: | |
Db        361 TAEAYNLAAAASAKDIYYNNMEEVCGGEKPYLSPDILEE---KHCEFKQLALDHFKKTKK 417

Qy        370 -SFKDVDQSFQKELETLLDAKQNDICKRN 397
               ||    :|:|||  :     :  || |
Db        418 MGGKDFSFRYQQELEEEIKELYENFCKHN 446


RESULT 7
A84810
probable guanylate binding protein [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004
C;Accession: A84810
R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J
Nature 402, 761-768, 1999
A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A;Reference number: A84420; MUID:20083487; PMID:10617197
A;Accession: A84810
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-217 <STO>
A;Cross-references: UNIPROT:Q8S8C8; GB:AE002093; NID:g6598487; PIDN:AAC79624.2; GSPDB:GN
C;Genetics:
A;Gene: At2g38840
A;Map position: 2

  Query Match             7.1%;  Score 216;  DB 2;  Length 217;
  Best Local Similarity   40.9%;  Pred. No. 3.5e-05;
  Matches   47;  Conservative   26;  Mismatches   36;  Indels    6;  Gaps    3;

Qy         20 QLKVNQEALEILSAITQPVVVVAIVGLYRTGKSYLMNKLAGKN--KGFSVASTVQSHTKG 77
              :|::::| || :| || |:  ||::| ||:|||:|:|:|   :  :|| |     : |||
Db         28 KLQLSREGLEAISRITTPISAVAVIGPYRSGKSFLLNQLLSLSCYEGFGVGHMRDTKTKG 87

Qy         78 IWIWCVP---HPNWPNHTLVLLDTEGLGDVEKADNKNDIQIFALALLLSSTFVYN 129
              ||:|  |      :    ::: |||||   | |: |  | :|||||  ::||  :||
Db         88 IWVWGTPLELEIDGVKTSVIYLDTEGFESVGKS-NVYDDRIFALATVMSSVLIYN 141


RESULT 8
H86168
hypothetical protein [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C;Accession: H86168
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,
 Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;
ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali,
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Reference number: A86141; MUID:21016719; PMID:11130712
A;Accession: H86168
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-991 <STO>
A;Cross-references: UNIPROT:Q9ZWA5; GB:AE005172; NID:g4204314; PIDN:AAD10695.1; GSPDB:GN
C;Genetics:
A;Map position: 1

  Query Match             7.0%;  Score 213.5;  DB 2;  Length 991;
  Best Local Similarity   18.2%;  Pred. No. 0.00032;
  Matches  124;  Conservative  133;  Mismatches  230;  Indels  193;  Gaps   26;

Qy         18 NEQLKVNQEALEILSAITQPVVVVAIVGLYRTGKSYLMNKLAGKNKGFSVASTVQSHTKG 77
              | :|| : ||:  |  :  || ||:: |    |||:: |:|  :: || | :  :
Db         20 NGKLKTDPEAIGALQKLKGPVAVVSLFGKALQGKSFIWNQLLSRSIGFEVQTLHRPCNGD 79

Qy         78 IWIWCVP----HPNWPNHTLVLLDTEGLGDVEKADNKNDIQIFALALLLSSTFVYNTVNK 133
              ||:|  |       :   ::|||||  |     :| | :   : :  :||
Db         80 IWMWIEPVKRISEDGTEYSLVLLDVE----LEDAKSIPTLGLNDIAL------------- 122

Qy        134 IDQGAIDLLHNVTELTDLLKARNSPDLDRVEDPA--DSASFFPDLVWTLRDFCLGLEIDG 191
                        :|: ||: |    :   :|    :   | | |  : |        |
Db        123 ------------DLSRLLEIRKQDHVGEAKDNTFFELGQFSPMFVQLMMDINSETVEGG 169

Qy        192 QLVTPD-----------------EYLENSLRPKQGSD---------------QRVQNF 217
              : || :                  :::   :||||  |                : | |
Db        170 EDVTQNSKLKKLRPLLLYGVDALMKFVSERVRPKQRGDTIVTGPPLAGFTKAFSENVNNN 229

Qy        218 NLPRLC----IQKFFPKKKCFIFDLPAHQKKLAQLETLPDDELEPE-----FVQQVTEFC 268
              :|::       :    ::        :   | : || ||: :  |       |: :| ||
Db        230 IVPKISSLWQTVEELEGRRARDTATEVYMSSLERSET-PDESMLLEAHNKAVVEALTAFC 288

Qy        269 SYIFSHSMTKTLPGGIMVNGSRLKNLVLTYVNAISSGD---------------------- 306
                  ::  | : |      ::|    :  |:
Db        289 ---------ESSIGNVEVKQKYKRDLWSFFAKALEDHKRVANVEAYSRCCNAIEDMGKKL 339

Qy        307 --LPCIENAVLALAQRENSAAVQKAIAHYDQQMG-----QKV-QLPMETLQELLDLHRTS 358
                |||  ::| :     :   |:  |:| |:  :      ||:     |::|::| :||
Db        340 WALPCSQDANIG----DMIKALDTAVAEYEASINGPMKWQKLSSFLRESVQDIL-VHRRG 394

Qy        359 ---------------EREAIEVFMKNSFKDVD------QSFQKELETLLDAKQNDICKRN 397
```

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                     :::::|  |    | ::      : :||  |: :|    ||||
Db        395 NQMDELMSENSKLKLQQQSLESTMNLLKKQLEGREKMNKEYQKRYESAID----DICK-- 448

Qy        398 LEASSDYCSALLKDIFGPLEEAVKQGIYSKPGGHNLFIQKTEELKAKYYREPRKGIQAEE 457
                ||     : |:     |:  : |: :   |:  ::      :           ::| |
Db        449 ---LSDQFKNRINDL-----ESKCKSIHDE---HSNLMEVLGSTR----------LEASE 487

Qy        458 VLQKY--LKSKESVSHAILQTDQALTETEKKKKEAQVKAE----AEKAEAQRLAAIQRQN 511
               :||     :  ||:  :  | ::|     |  : ::|  |     :||  :::||:: :
Db        488 WKRKYEGTLDENGVSNIRVGVDASITRCSNKLIDWKIKYENTVSEQKAVTEKIAAMEEKL 547

Qy        512 EQ--------------MMQERERLHQEQVRQMEIAKQNWLAEQQKMQEQQMQVFINCFIS 557
               :|              :: |:|::  |:  ::   :|   : : ::::  ::|   |
Db        548 KQASTTEDGLRAEFSRVLDEKEKIITEKAAKLATLEQQLASTRAELKKSALKV-DECSSE 606

Qy        558 PLPVTMRVCSSGKEGEAARS 577
                | :::    :: |: :|
Db        607 AKDVRLQMSLLNEKYESVKS 626


RESULT 9
G02520
plectin - human
C;Species: Homo sapiens (man)
C;Date: 21-Dec-1996 #sequence_revision 06-Jun-1997 #text_change 20-Aug-1999
C;Accession: G02520
R;McLean, W.H.I.; Smith, F.J.D.
submitted to the EMBL Data Library, March 1996
A;Reference number: H01385
A;Accession: G02520
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-4574 <MCL>
A;Cross-references: EMBL:U53204; NID:g1477645; PIDN:AAB05427.1; PID:g1477646
C;Genetics:
A;Gene: PLEC1
C;Superfamily: plectin; alpha-actinin actin-binding domain homology; ribosomal protein S
F;68-283/Domain: alpha-actinin actin-binding domain homology <ACT>

  Query Match           5.6%;  Score 171.5;  DB 2;  Length 4574;
  Best Local Similarity   18.7%;  Pred. No. 0.46;
  Matches   81;  Conservative   79;  Mismatches  145;  Indels  129;  Gaps   12;

Qy        190 DGQLVTPDEYLENSLRPKQGSDQRVQNFNLPRLCIQKFFPKKKCFIFDLPAHQKKLAQLE 249
              | ::    :: | :|| |   :| :    |                :   ||| |
Db       2191 DAEMEKHKKFAEQTLRQKAQVEQELTTLRLQ--------------LEETDHQKNLL--- 2232

Qy        250 TLPDDELE------PEFVQQVTEFCSYIFSHSMTKTLPGGIMVNGSRLKNLVLTYVNAIS 303
                |:||:       |  :| ::    :||  :        |   |:||  :
Db       2233 ---DEELQRLKAEATEAARQRSQVEEELFSVRVQ-------MEELSKLKARIEA------ 2276

Qy        304 SGDLPCIENAVLALAQRENSAAVQKAIAHYDQQMGQKVQLPMETLQELLDLHRTSE---- 359
                ||  | |  ::|:    :  |   :|: ::        ||   | : :|
Db       2277 -------ENRALILRDKDNTQRFLQEEAEKMKQVAEEAARLSVAAQEAARLRQLAEEDLA 2329

Qy        360 --REAIEVFMKNSFKDVDQSFQKELETLLDAKQNDICKRNLEASSDYCSALLKDIFGPLE 417
                |    |  :|   : | :: : : |         :: ::  | : :    | :|     :
Db       2330 QQRALAEKMLKEKMQAVQEATRLKAEA-------ELLQQQKELAQEQARRLQED-----K 2377

Qy        418 EAVKQGIYSKPGGHNLFIQ-----------KTEELKAKYYREPRKGIQAEEVLQKYLKSK 466
              | : | :  :  |     ::           : | || :      |   :|||  |:: |
Db       2378 EQMAQQLAEETQGFQRTLEAERQRQLEMSAEAERLKLRVAEMSRAQARAEEDAQRFRKQA 2437

Qy        467 ESVSHAILQTD----------------------------QALTETEKKKKEAQVKAEAEK 498
              | :   : :|:                          :|: | |::|:: | :|:  :
Db       2438 EEIGEKLHRTELATQEKVTLVQTLEIQRQQSDHDAERLREAIAELEREKEKLQQEAKLLQ 2497

Qy        499 AEAQRLAAIQRQNEQMMQERERLHQ----------------------EQVRQMEIAKQN 535
               ::: :  :|:  ||::|| : | |                      ||: | |:||
Db       2498 LKSEEMQTVQQ--EQLLQETQALQQSFLSEKDSLLQRERFIEQEKAKLEQLFQDEVAKAQ 2555

Qy        536 WLAEQQKMQEQQMQ 549
               | |:|: |:|||:
Db       2556 QLREEQQRQQQQME 2569


RESULT 10
A59404
plectin [imported] - human
C;Species: Homo sapiens (man)
C;Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 09-Jul-2004
C;Accession: C59404; A59404
R;Liu, C.G.; Maercker, C.; Castanon, M.J.; Hauptmann, R.; Wiche, G.
Proc. Natl. Acad. Sci. U.S.A. 93, 4278-4283, 1996
A;Title: Human plectin: organization of the gene, sequence analysis, and chromosome loc
A;Reference number: C59404; MUID:96210632; PMID:8633055
A;Accession: C59404
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-4684 <STO>
A;Cross-references: UNIPROT:Q15149; GB:CAA91196; NID:g1296662; PIDN:CAA91196.1
C;Superfamily: plectin; alpha-actinin actin-binding domain homology; ribosomal protein

  Query Match           5.6%;  Score 171.5;  DB 2;  Length 4684;
  Best Local Similarity   18.7%;  Pred. No. 0.48;
  Matches   81;  Conservative   79;  Mismatches  145;  Indels  129;  Gaps   12;

Qy        190 DGQLVTPDEYLENSLRPKQGSDQRVQNFNLPRLCIQKFFPKKKCFIFDLPAHQKKLAQLE 249
              | ::    :: | :|| |   :| :    |                :   ||| |
Db       2301 DAEMEKHKKFAEQTLRQKAQVEQELTTLRLQ--------------LEETDHQKNLL--- 2342

Qy        250 TLPDDELE------PEFVQQVTEFCSYIFSHSMTKTLPGGIMVNGSRLKNLVLTYVNAIS 303
                |:||:       |  :| ::    :||  :        |   |:||  :
Db       2343 ---DEELQRLKAEATEAARQRSQVEEELFSVRVQ-------MEELSKLKARIEA------ 2386

Qy        304 SGDLPCIENAVLALAQRENSAAVQKAIAHYDQQMGQKVQLPMETLQELLDLHRTSE---- 359
                ||  | |  ::|:    :  |   :|: ::        ||   | : :|
Db       2387 -------ENRALILRDKDNTQRFLQEEAEKMKQVAEEAARLSVAAQEAARLRQLAEEDLA 2439

Qy        360 --REAIEVFMKNSFKDVDQSFQKELETLLDAKQNDICKRNLEASSDYCSALLKDIFGPLE 417
                |    |  :|   : | :: : : |         :: ::  | : :    | :|     :
Db       2440 QQRALAEKMLKEKMQAVQEATRLKAEA-------ELLQQQKELAQEQARRLQED-----K 2487

Qy        418 EAVKQGIYSKPGGHNLFIQ-----------KTEELKAKYYREPRKGIQAEEVLQKYLKSK 466
              | : | :  :  |     ::           : | || :      |   :|||  |:: |
Db       2488 EQMAQQLAEETQGFQRTLEAERQRQLEMSAEAERLKLRVAEMSRAQARAEEDAQRFRKQA 2547

Qy        467 ESVSHAILQTD----------------------------QALTETEKKKKEAQVKAEAEK 498
              | :   : :|:                          :|: | |::|:: | :|:  :
Db       2548 EEIGEKLHRTELATQEKVTLVQTLEIQRQQSDHDAERLREAIAELEREKEKLQQEAKLLQ 2607

Qy        499 AEAQRLAAIQRQNEQMMQERERLHQ----------------------EQVRQMEIAKQN 535
               ::: :  :|:  ||::|| : | |                      ||: | |:||
Db       2608 LKSEEMQTVQQ--EQLLQETQALQQSFLSEKDSLLQRERFIEQEKAKLEQLFQDEVAKAQ 2665

Qy        536 WLAEQQKMQEQQMQ 549
               | |:|: |:|||:
Db       2666 QLREEQQRQQQQME 2679


RESULT 11
T22382
hypothetical protein F48F5.1 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T22382
R;Lloyd, C.
submitted to the EMBL Data Library, November 1996
A;Reference number: Z19558
A;Accession: T22382
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-1291 <WIL>
A;Cross-references: UNIPROT:Q9XV10; EMBL:Z81541; PIDN:CAB04411.1; GSPDB:GN00023; CESP:F4
A;Experimental source: clone F48F5
C;Genetics:
```

```
A;Gene: CESP:F48F5.1
A;Map position: 5
A;Introns: 753/2; 814/3; 987/2; 1030/3; 1114/2; 1153/3; 1222/3

  Query Match             5.3%;  Score 160.5;  DB 2;  Length 1291;
  Best Local Similarity   18.7%;  Pred. No. 0.38;
  Matches  143;  Conservative  100;  Mismatches  224;  Indels  299;  Gaps   31;

Qy         14 IENFNEQLK------------VNQEALEILSAITQPVVVVAIVGLYRTGKSYLMNKLAG 60
Db        287 LSRVNEKLKSTFPADNARQVQSFNQFKEESFSVPTDAVSAVGVLAEYKK-----CNHLGG 341

Qy         61 ------KNKGFSVASTVQSHTKGIWIWCVPHPNWPNHTLVLL----DTEGLGDVEKADNK 110
Db        342 PQTDDERRPGHEFMAKVKS--------------VGDSLIALHMFSQTLALDQLEK---- 382

Qy        111 NDIQIFALAL--------LLSSTFVYNTVNKIDQGA--IDLLHNVTELTDLLKARNSPDL 160
Db        383 -DVADFVKSLTFTDINNQTLSEGEIVKVVEDIKKSGKLAKIQENVKSIEDKINGIKLKNL 441

Qy        161 DRVEDPADSASFFPDLVWTLRDFCLGLEIDGQLVTPDEYLENSLRPKQGSDQRVQNFNLP 220
Db        442 ESTLLPNLNNSFIQDVMFK------------EVITAETSVSG------------------ 471

Qy        221 RLCIQKFFPKKKCFIFDLPAHQKKLAQLETLPDDELEPEFVQQVTEFCSYIFSHSM--TK 278
Db        472 --CLQK-LKAKSLLVTQAIATIQKLRKL----DDKL-LESVQQTAKSVSQ-FSETLASVK 522

Qy        279 TLPGGIMVNGSRLKNLVLTYVNAISSGDLPCIENAVLALAQRENSAAVQKAIAH------ 332
Db        523 KIPDAMKKN----------------------VKNVTLELNKRSESLNQSDAISHSASALR 560

Qy        333 -------YDQQMGQ------------KVQLPME--TLQELLDLHRTS--EREAIEVFMK 368
Db        561 SVFGLVKLESSIGQLNDTDTIVSSEIDKIKIPAEKMKLQKLWGNHTEGMVSLQAAVVQAK 620

Qy        369 NSFKDVDQS----------FQKELETLLDAKQ---------------------------- 390
Db        621 AFVAKIDVSKLKTLNNYSAILKTLETMPDVKMEALEKSEVLEILIRAISATRRRRRRAAG 680

Qy        391 ------------NDICKRNLEASSDYC------------SALLKDIFGPLEEAVKQGIYS 426
Db        681 SNAHLVAAKVILDKIAALDLQFSSNIAHFKNAPLAFQSFSKFLAKFF-----ATQQKISA 735

Qy        427 KPGG-------------------------------------------------HNLFI 435
Db        736 SQNGGGGGGGSGESEFPTVIVVVSIVGALLLALAAFLAFLVYGFHQRKKQAKIDRDNKEI 795

Qy        436 QKTEELKAKYYREPRKGIQAEE-VLQKYLKSKESVSHAI--------------LQTDQAL 480
Db        796 RDEIEMEARQAEENEQRIAAEKNALEAKIKEKSNMRKVVDEQNQREKDELQAKLRADQEK 855

Qy        481 TETEK-----------KKKEAQVKAEAEKAEAQRLAAIQRQNEQMMQERERLHQEQVRQM 529
Db        856 SEARKIAEKKKDEQNQKEKEAKLRADQEKSEARKVAE-KKKDEQNQKEKDKLQAKLRADQ 914

Qy        530 EIAKQNWLAEQQKMQEQQMQVFINCF--ISPLP-VTMRVCSSGKEG 572
Db        915 EKSEARKIAEKKKKEEDEAQKVKNIWKHIKKMRFTTLRACADFIEG 960


RESULT 12
T13030
microtubule binding protein D-CLIP-190 - fruit fly (Drosophila melanogaster)
C;Species: Drosophila melanogaster
C;Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 17-Nov-2000
C;Accession: T13030
R;Lantz, V.A.; Miller, K.G.
J. Cell Biol. 140, 897-910, 1998
A;Title: A class VI unconventional myosin is associated with a homologue of a microtubul
A;Reference number: Z17588; MUID:98139549; PMID:9472041
A;Accession: T13030
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-1690 <LAN>
A;Cross-references: EMBL:AF041382; NID:g2773362; PID:g2773363; PIDN:AAB96783.1
A;Experimental source: strain Oregon R
C;Genetics:
A;Cross-references: FlyBase:FBgn0020503
C;Keywords: cytoskeleton

  Query Match             5.3%;  Score 160.5;  DB 2;  Length 1690;
  Best Local Similarity   20.8%;  Pred. No. 0.54;
  Matches  114;  Conservative   90;  Mismatches  185;  Indels  159;  Gaps   26;

Qy        104 VEKADNKNDIQIFALALLLSSTFVYNTVNKIDQGAIDL---LHNVTELTDLLKARNSPDL 160
Db        385 VERDLDREDAQNQALQL-------QKNINELKARIVELESALGNERKKTEELQC----SI 433

Qy        161 DRVEDPADSASFFPDLVWTLRDFCLGLEIDGQLVTPDEYLENSLRPKQGSDQRVQNFNLP 220
Db        434 DEAQ-----------------FC-GDELNAQSQVYKEKIHD-------LESKITKLVSA 467

Qy        221 RLCIQKFFPKKKCFIFDLP----AHQKKLAQLE---TLPDDELEPEFVQQ------VTEF 267
Db        468 TPSLQSILPP------DLPSDDGALQEEIAQLQEKMTIQQKEVESRIAEQLEEEQRLREN 521

Qy        268 CSYIFSHSMTKTLPGGIMVNGSRLKNLVLTYVNAISSGDLPC-IEN--AVLALAQRENSA 324
Db        522 VKYL--NEQIATLQSELVSKDEALEKFSLS----------ECGIENLRRELALLKEENEK 569

Qy        325 AVQKAIAHYDQQMGQKVQLPMETLQELLDLHRTS---EREAI-----------EVFMKN- 369
Db        570 QAQEAQAEFTRKLAEKSVEVLRLSSELQNLKATSDSLESERVNKSDECEILQTEVRMRDE 629

Qy        370 SFKDVDQSFQKELETLLDAKQNDICKRNLEASSDYCSALLKDIFGPLEEAVKQGIYSKPG 429
Db        630 QIRELNQQLD-EVTTQLNVQKAD------------SSALDDML----RLQKEGTEEK-- 669

Qy        430 GHNLFIQKTEELKAKYYREPRKGIQAEEVLQKYLK------------------------ 464
Db        670 --STLLEKTEKELVQIKEQAAKTLQDKEQLEKQISDLKQLAEQEKLVREKTENAINQIQL 727

Qy        465 SKESVSHAILQTDQALTETEKKKKEAQVKAEAEKAE-----------AQRLAAIQRQNEQ 513
Db        728 EKESIEQQLALKQNELEDFQKKQSESEVHLQEIKAQNTQKDLELVESGESLKKLQQQLEE 787

Qy        514 MMQERERLHQEQVRQMEIAKQNWLAEQQKMQE-QQMQVFINCFISPLPVT--------MR 564
Db        788 KTLGHEKL---QAALEELKKEKETIIKEKEQELQQLQSKSAESESALKVVQVQLEQLQQQ 844

Qy        565 VCSSGKEG 572
Db        845 AAASGEEG 852


RESULT 13
A39638
plectin - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C;Accession: A39638; S21876
R;Wiche, G.; Becker, B.; Luber, K.; Weitzer, G.; Castanon, M.J.; Hauptmann, R.; Stratowa
J. Cell Biol. 114, 83-99, 1991
A;Title: Cloning and sequencing of rat plectin indicates a 466-kD polypeptide chain with
A;Reference number: A39638; MUID:91268156; PMID:2050743
A;Accession: A39638
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-4687 <WIC>
A;Cross-references: UNIPROT:P30427; EMBL:X59601; NID:g1292885; PIDN:CAA42169.1; PID:g156
C;Superfamily: plectin; alpha-actinin actin-binding domain homology; ribosomal protein S
C;Keywords: cytoskeleton; transmembrane protein
F;6-103/Domain: ribosomal protein S10 homology <RS10>
F;184-399/Domain: alpha-actinin actin-binding domain homology <ACT>
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Query Match 5.3%; Score 160.5; DB 1; Length 4687;
Best Local Similarity 18.3%; Pred. No. 1.9;
Matches 80; Conservative 79; Mismatches 143; Indels 135; Gaps 13;

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Qy      190 DGQLVTPDEYLENSLRPKQGSDQRVQNFNLPRLCIQKFFPKKKCFIFDLPAHQKKLAQLE 249
Db     2304 DAEMEKHKKFAEQTLRQKAQVEQELTTLRLQ--------------LEETDHQKSIL--- 2345

Qy      250 TLPDDELE------PEFVQQVTEFCSYIFSHSMTKTLPGGIMVNGSRLKNLVLTYVNAIS 303
Db     2346 ---DEELQRLKAEVTEAARQRSQVEEELFS----------VRVQMEELGKL-KARIEA-- 2389

Qy      304 SGDLPCIENAVLALAQRENSAAVQKAIAHYDQQMGQKVQLPMETLQELLDLHRTSE---- 359
Db     2390 -------ENRALILRDKDNTQRFLEEEAEKMKQVAEEAARLSVAAQEAARLRQLAEEDLA 2442

Qy      360 --REAIEVFMKNSFKDVDQSFQKELETLLDAKQNDICK---RNLEASSDYCSALLKDIFG 414
Db     2443 QQRALAEKMLKEKMQAVQEATRLKAEAELLQQQKELAQEQARRLQAD------------- 2489

Qy      415 PLEEAVKQGIYSKPGGHNLFIQ----------KTEELKAKYYREPRKGIQAEEVLQKYL 463
Db     2490 --KEQMAQQLVEETQGFQRTLEAERQRQLEMSAEAERLKLRMAEMSRAQARAEEDAQRFR 2547

Qy      464 KSKESVSHAILQTD----------------------------QALTETEKKKKEAQVKAE 495
Db     2548 KQAEEIGEKLHRTELATQEKVTLVQTLEIQRQQSDQDAERLREAIAELEREKEKLKQEAK 2607

Qy      496 AEKAEAQRLAAIQRQNEQMMQERERLHQ----------------------EQVRQMEIA 532
Db     2608 LLQLKSEEMQTVQQ--EQILQETQALQKSFLSEKDSLLQRERFIEQEKAKLEQLFQDEVA 2665

Qy      533 KQNWLAEQQKMQEQQMQ 549
Db     2666 KAKQLQEEQQRQQQQME 2682
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RESULT 14
T49593
hypothetical protein B3E4.60 [imported] - Neurospora crassa
C;Species: Neurospora crassa
C;Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 09-Jul-2004
C;Accession: T49593
R;Schulte, U.; Aign, V.; Hoheisel, J.; Brandt, P.; Fartmann, B.; Holland, R.; Nyakatura,
submitted to the Protein Sequence Database, May 2000
A;Reference number: Z25022
A;Accession: T49593
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-862 <SCH>
A;Cross-references: UNIPROT:Q9P5X6; EMBL:AL355931; GSPDB:GN00116; NCSP:B3E4.60
A;Experimental source: BAC clone B3E4; strain OR74A
C;Genetics:
A;Gene: NCSP:B3E4.60
A;Map position: 6
A;Introns: 181/2; 764/1
C;Superfamily: Saccharomyces cerevisiae probable membrane protein YOR165w

Query Match 5.2%; Score 159.5; DB 2; Length 862;
Best Local Similarity 19.4%; Pred. No. 0.26;
Matches 126; Conservative 102; Mismatches 228; Indels 193; Gaps 27;

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Qy       14 IENFNEQLKVNQEALEILSAITQPVV-----VVAIVGLYRTGKSYLMNKLAGKNKGFSVA 68
Db       27 IQVINEDKQYNTNLNEYLNETHVAEAGFNYHLISVFGSQSTGKSTLLNHLFGTQ--FSVM 84

Qy       69 STVQSH--TKGIWIWCVPHPNWPNHTLVLLDTEGLGDVEKADNKNDIQIFAL-ALLLSST 125
Db       85 SERERRQTTKGIWMSKNKNEGKMADNILVMDVEGTDGRERGEDQDFERKSALFALATSEV 144

Qy      126 FVYNTVNK---IDQGA-IDLLHNVTELTDLLKARNSPDLDRVEDPADSASFFPDLVWTLR 181
Db      145 LIVNIWEHQVGLYQGANMGLLKTVFEVNMQLFLKDKQNQTR------SLLFF-----VIR 193
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Qy      182 DFCLGLEIDGQLVTPDEYLENSL------------RPKQGSDQRVQNFNLPRLCIQKFFP 229
Db      194 DH-IG-------VTPLANLRNTLIQDLTHIWSSISKPAGLENSKIEDY------------ 233

Qy      230 KKKCFIFDLPAHQKKLAQLETLPDDELEPEFVQQVTEFCSYIFSHSMTKTLPGGIMVNGS 289
Db      234 ----FDFAFAALPHKILQ----PD-----KFISEVQNL--------------GSRFIAGH 266

Qy      290 RLKNLVLTYVNAISSGDLPCIENAVLALAQRENSAAVQKAIAHYDQQMGQKVQLPMETLQ 349
Db      267 RNKD-----------------------------------SDATDDQELTGGVFLP----- 286

Qy      350 ELLDLHRTSEREAIEVFMKN------SFKDVDQSFQKELETLLDAKQNDICKRNLEASSD 403
Db      287 ---EYHRRIPADGLSIYAEGIWDQIVSNKDLDLPTQQE---LLAQFRCDEIAREVQIAFD 340

Qy      404 YCSALLKDIFGPLEEAVKQGIYSKPG-----GHNLFIQKTEELKAKYYR--EPRKGIQAE 456
Db      341 AAIAPLEEQQAESTRAGKPAVLPNLGQIGAEAREKCVKNFETQASRYHKGVYTTKRAELE 400

Qy      457 EVLQKYLKS-----------------KESVSHAILQTDQA--------LTETEKKKKEAQ 491
Db      401 DKIDNRLKALYQAHLTAAHKAGVTAFSEAVANAVKAGQKAGGAYEFAEIVEKQKTKTLEI 460

Qy      492 VKAEAEKAEAQRLAAIQRQNEQMMQERE------RLHQEQVRQMEIAKQNWLAEQQKMQE 545
Db      461 FKKEAQSLAIPGVAWSNFKPQYLIFEKELDEVSARLRKEEMRRLAIRVERWVKSR----- 515

Qy      546 QQMQVFINCFISPLPVTMRVCSSGKEGEAARSCG----SQQGVWSQKVW 590
Db      516 ---------LGDAIGLEFNKLGSGRGGSGAPESGEKPATEKDIW-DRVW 554
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RESULT 15
H90279
microtubule binding protein, probable [imported] - Sulfolobus solfataricus
C;Species: Sulfolobus solfataricus
C;Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 09-Jul-2004
C;Accession: H90279
R;She, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Awayez, M.J.; Chan-
Jong, I.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder, P
arrett, R.A.; Ragan, M.A.; Sensen, C.W.; Van der Oost, J.
submitted to GenBank, April 2001
A;Description: Sulfolobus solfataricus complete genome.
A;Reference number: A99139
A;Accession: H90279
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-464 <KUR>
A;Cross-references: UNIPROT:Q9UXN4; GB:AE006641; NID:g13814451; PIDN:AAK41495.1; GSPDB:G
C;Genetics:
A;Gene: SSO1256

Query Match 5.2%; Score 158; DB 2; Length 464;
Best Local Similarity 23.0%; Pred. No. 0.14;
Matches 85; Conservative 81; Mismatches 136; Indels 68; Gaps 17;

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Qy      251 LPDDEL-----EPEFVQQVTEFCSYIFSH---SMTKTLPGGIMVNGSRLKNLVLTYVNAI 302
Db        2 LKDDILKLLKEDAEFRKQVEEILGISFINVTLADLKDILKGLLASMDKLKSSVDQLVDAQ 61

Qy      303 SSGD--LPCIENAV--LALAQRENSAAVQKAIAHYDQQMGQKVQLPMETLQELLDLHRTS 358
Db       62 RRAEERIAKLENAVEQLVEAQKRTDERITKL-----EESTKKLE---QAVQELIEAQKKH 113

Qy      359 EREAIEVFMKNSFKDVDQSFQKELETLLDAKQNDICKRNLEASSDYCSALLKDIFGPLEE 418
Db      114 DERITK--LEESTKKLEQAVQELIEA---QKKHDERITKLEESTK-----------KLEQ 157

Qy      419 AVKQGIYSKPGGHNLFIQKTEELKAKYYREPRKGIQAEEVLQKYLKSKESVSHAILQTDQ 478
Db      158 AVQELIEAQK-KHDERITKLEESTKKLEQAVQELIEAQKKHDERITKLEESTKKLEQAVQ 216
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Qy        479 ALTETEKKKKE--------------AQVKAEAEKAEAQRLAAIQRQNEQMMQERERLHQ 523
              | | :||  |                |   ||:|   :|:  :: :: | : : :|  :
Db        217 ELIEAQKKHDERITKLEESTKKLEQAVQELIEAQKKHDERITKLE-ESIQKLVDAQRRAE 275

Qy        524 EQVRQMEIAKQNWLAEQQKMQEQQMQVFINCFISPL-PVTMRVCSS--GKEG---EAARS 577
              |:: ::| | :  | | ||  :::        |: |  |||::  |  | :    |  ::
Db        276 ERIAKLENAVEQ-LVEAQKRTDER--------ITKLEEVTMKLVESQLGMQNEIRELRKA 326

Qy        578 CGSQQGVWSQ 587
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Db        327 LGSMGKRWGR 336
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Search completed: July 9, 2005, 13:25:47
Job time : 22 secs

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: July 9, 2005, 13:19:44 ; Search time 43 Seconds
(without alignments)
1025.991 Million cell updates/sec

Title: US-10-659-549-3
Perfect score: 3043
Sequence: 1 MALEIHMSDPMCLIENFNEQ.....GEAARSCGSQQGVWSQKVWV 591

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
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6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	3043	100.0	591	4	US-09-643-657-3	Sequence 3, Appli
2	2610.5	85.8	633	2	US-08-736-770-3	Sequence 3, Appli
3	1966.5	64.6	605	4	US-09-949-016-8823	Sequence 8823, Ap
4	1958.5	64.4	592	2	US-08-736-770-6	Sequence 6, Appli
5	1958.5	64.4	592	4	US-09-702-705-1809	Sequence 1809, Ap
6	1958.5	64.4	592	4	US-09-736-457-1809	Sequence 1809, Ap
7	1958.5	64.4	592	4	US-09-643-657-4	Sequence 4, Appli
8	1958.5	64.4	592	4	US-09-671-325-1809	Sequence 1809, Ap
9	1897	62.3	591	2	US-08-736-770-5	Sequence 5, Appli
10	1897	62.3	591	4	US-09-643-657-5	Sequence 5, Appli
11	1881	61.8	608	2	US-08-736-770-1	Sequence 1, Appli
12	1832.5	60.2	583	4	US-09-949-016-8267	Sequence 8267, Ap
13	1765.5	58.0	589	4	US-09-643-657-14	Sequence 14, Appl
14	1757.5	57.8	591	4	US-09-643-657-15	Sequence 15, Appl
15	1459.5	48.0	620	4	US-09-643-657-13	Sequence 13, Appl
16	932.5	30.6	573	4	US-09-643-657-18	Sequence 18, Appl
17	526	17.3	147	4	US-09-370-838-99	Sequence 99, Appl
18	526	17.3	147	4	US-09-854-133-99	Sequence 99, Appl
19	509	16.7	159	4	US-09-370-838-98	Sequence 98, Appl
20	509	16.7	159	4	US-09-854-133-98	Sequence 98, Appl
21	392	12.9	96	4	US-09-513-999C-5037	Sequence 5037, Ap
22	296	9.7	103	4	US-09-643-657-16	Sequence 16, Appl
23	239	7.9	64	4	US-09-643-657-17	Sequence 17, Appl
24	203	6.7	57	4	US-09-621-976-4483	Sequence 4483, Ap
25	197	6.5	573	4	US-09-270-767-44491	Sequence 44491, A
26	154.5	5.1	1427	4	US-09-538-092-1044	Sequence 1044, Ap
27	151	5.0	1180	4	US-09-543-681A-6436	Sequence 6436, Ap
28	148	4.9	710	4	US-09-107-532A-5067	Sequence 5067, Ap
29	148	4.9	1288	4	US-09-919-039-209	Sequence 209, App
30	146.5	4.8	1531	4	US-09-418-710-29	Sequence 29, Appl
31	146.5	4.8	1531	4	US-09-839-479-29	Sequence 29, Appl
32	145.5	4.8	568	4	US-09-949-016-10580	Sequence 10580, A
33	144	4.7	1857	4	US-09-917-254-91	Sequence 91, Appl
34	144	4.7	1972	4	US-09-538-092-1084	Sequence 1084, Ap
35	144	4.7	1984	4	US-09-949-016-7111	Sequence 7111, Ap
36	144	4.7	1984	4	US-09-949-016-7112	Sequence 7112, Ap
37	144	4.7	1984	4	US-09-949-016-7113	Sequence 7113, Ap
38	142	4.7	1972	4	US-08-875-435B-4	Sequence 4, Appli
39	141.5	4.7	1527	4	US-09-418-710-27	Sequence 27, Appl
40	141.5	4.7	1527	4	US-09-839-479-27	Sequence 27, Appl
41	140.5	4.6	897	1	US-08-095-737-4	Sequence 4, Appli
42	140.5	4.6	897	1	US-08-480-145-4	Sequence 4, Appli
43	140.5	4.6	897	2	US-08-477-389-4	Sequence 4, Appli
44	140.5	4.6	1540	4	US-09-949-016-7037	Sequence 7037, Ap
45	140.5	4.6	2107	4	US-09-949-016-7646	Sequence 7646, Ap

ALIGNMENTS

RESULT 1
US-09-643-657-3
; Sequence 3, Application US/09643657
; Patent No. 6642024
; GENERAL INFORMATION:
; APPLICANT: Diane Pennica
; TITLE OF INVENTION: GUANYLATE-BINDING PROTEIN
; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/643,657
; FILING DATE: 17-Aug-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/015,089A
; FILING DATE: 29-Jan-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Hasak, Janet E.
; REGISTRATION NUMBER: 28,616
; REFERENCE/DOCKET NUMBER: P1056
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1896
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 591 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-09-643-657-3

Query Match 100.0%; Score 3043; DB 4; Length 591;
Best Local Similarity 100.0%; Pred. No. 1.7e-254;
Matches 591; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 MALEIHMSDPMCLIENFNEQLKVNQEALEILSAITQPVVVVAIVGLYRTGKSYLMNKLAG 60
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Qy          61 KNKGFSVASTVQSHTKGIWIWCVPHPNWPNHTLVLLDTEGLGDVEKADNKNDIQIFALAL 120
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Db          61 KNKGFSVASTVQSHTKGIWIWCVPHPNWPNHTLVLLDTEGLGDVEKADNKNDIQIFALAL 120

Qy         121 LLSSTFVYNTVNKIDQGAIDLLHNVTELTDLLKARNSPDLDRVEDPADSASFFPDLVWTL 180
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         121 LLSSTFVYNTVNKIDQGAIDLLHNVTELTDLLKARNSPDLDRVEDPADSASFFPDLVWTL 180

Qy         181 RDFCLGLEIDGQLVTPDEYLENSLRPKQGSDQRVQNFNLPRLCIQKFFPKKKCFIFDLPA 240
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         181 RDFCLGLEIDGQLVTPDEYLENSLRPKQGSDQRVQNFNLPRLCIQKFFPKKKCFIFDLPA 240

Qy         241 HQKKLAQLETLPDDELEPEFVQQVTEFCSYIFSHSMTKTLPGGIMVNGSRLKNLVLTYVN 300
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy         301 AISSGDLPCIENAVLALAQRENSAAVQKAIAHYDQQMGQKVQLPMETLQELLDLHRTSER 360
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Qy         361 EAIEVFMKNSFKDVDQSFQKELETLLDAKQNDICKRNLEASSDYCSALLKDIFGPLEEAV 420
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Qy         421 KQGIYSKPGGHNLFIQKTEELKAKYYREPRKGIQAEEVLQKYLKSKESVSHAILQTDQAL 480
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Qy         481 TETEKKKKEAQVKAEAEKAEAQRLAAIQRQNEQMMQERERLHQEQVRQMEIAKQNWLAEQ 540
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy         541 QKMQEQQMQVFINCFISPLPVTMRVCSSGKEGEAARSCGSQQGVWSQKVWV 591
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RESULT 2
US-08-736-770-3
; Sequence 3, Application US/08736770
; Patent No. 5871965
;  GENERAL INFORMATION:
;    APPLICANT:  Bandman, Olga
;    APPLICANT:  Au-Young, Janice
;    APPLICANT:  Hillman, Jennifer L.
;    TITLE OF INVENTION:  NOVEL HUMAN GUANYLATE BINDING PROTEINS
;    NUMBER OF SEQUENCES:  6
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Incyte Pharmaceuticals, Inc.
;      STREET:  3174 Porter Drive
;      CITY:  Palo Alto
;      STATE:  CA
;      COUNTRY:  US
;      ZIP:  94304
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ Version 1.5
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/736,770
;      FILING DATE:  Filed Herewith
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Billings, Lucy J.
;      REGISTRATION NUMBER:  36,749
;      REFERENCE/DOCKET NUMBER:  PF-0145 US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415-855-0555
;      TELEFAX:  415-845-4166
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  633 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
;    IMMEDIATE SOURCE:
;      LIBRARY:
;      CLONE:  Consensus
US-08-736-770-3

  Query Match             85.8%;  Score 2610.5;  DB 2;  Length 633;
  Best Local Similarity   94.4%;  Pred. No. 4.8e-217;
  Matches  519;  Conservative    8;  Mismatches   20;  Indels    3;  Gaps    3;

Qy           1 MALEIHMSDPMCLIENFNEQLKVNQEALEILSAITQPVVVVAIVGLYRTGKSYLMNKLAG 60
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Db           1 MALEIHMSDPMCLIENFNEQLKVNQEALEILSAITQPVVVVAIVGLYRTGKSYLMNKLAG 60

Qy          61 KNKGFSVASTVQSHTKGIWIWCVPHPNWPNHTLVLLDTEGLGDVEKADNKNDIQIFALAL 120
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Db          61 KNKGFSVASTVQSHTKGIWIWCVPHPNWPNHTLFCL-TPRPGRC-KADNKNDIQIFALAL 118

Qy         121 LLSSTFVYNTVNKIDQGAIDLLHNVTELTDLLKARNSPDLDRVEDPADSASFFPDLVWTL 180
               ||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         119 LLSSTXVYNTVNKIDQGAIDLLHNVTELTDLLKARNSPDLDRVEDPADSASFFPDLVWTL 178

Qy         181 RDFCLGLEIDGQLVTPDEYLENSLRPKQGSDQRVQNFNL-PRLCIQKFFPKKKCFIFDLP 239
               :|||||||||||||||||||||||||||||||||||| | :  :  | ||: ||| ||
Db         179 KDFCLGLEIDGQLVTPDEYLENSLRPKQGSDQRVQNFNLTPSVVYRSSFQKKEWFIFXLP 238

Qy         240 AHQKKLAQLETLPDDELEPEFVQQVTEFCSYIFSHSMTKTLPGGIMVNGSRLKNLVLTYV 299
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Qy         300 NAISSGDLPCIENAVLALAQRENSAAVQKAIAHYDQQMGQKVQLPMETLQELLDLHRTSE 359
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Db         299 NAISSGDLPCMENAVLALAQRENSAAVQKAIAHYDQQMGQKVQLPTETLQELLDLHRDSE 358

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Qy         420 VKQGIYSKPGGHNLFIQKTEELKAKYYREPRKGIQAEEVLQKYLKSKESVSHAILQTDQA 479
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         419 VKQGIYSKPGGHNLFIQKTEELKAKYYREPRKGIQAEEVLQKYLKSKESVSHAILQTDQA 478

Qy         480 LTETEKKKKEAQVKAEAEKAEAQRLAAIQRQNEQMMQERERLHQEQVRQMEIAKQNWLAE 539
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         479 LTETEKKKKEAQVKAEAEKAEAQRLAAIQRQNEQMMQERERLHQEQVRQMEIAKQNWLAE 538

Qy         540 QQKMQEQQMQ 549
               ||||||||||
Db         539 QQKMQEQQMQ 548


RESULT 3
US-09-949-016-8823
; Sequence 8823, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
```

PR 24-AUG-2000; 2000WO-US023328.
PR 08-NOV-2000; 2000WO-US030952.
PR 10-NOV-2000; 2000WO-US030873.
XX
PA (GETH) GENENTECH INC.
XX
PI Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, Gao W;
PI Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;
PI Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;
XX
DR WPI; 2001-408281/43.
DR N-PSDB; AAS21266.
XX
PT Isolated , secretory and transmembrane PRO polypeptide used to detect
PT other PRO polypeptides, link bioactive molecules to cells expressing PRO
PT polypeptides, and detect the presence of mammalian tumors e.g. lung,
PT breast, prostate, cervical.
XX
PS Claim 12; Fig 46; 813pp; English.
XX
CC AAU12172-AAU12446 represent novel human secretory and transmembrane PRO
CC polypeptides. The PRO polypeptides are useful to detect other PRO
CC polypeptides, to link bioactive molecules to cells expressing PRO
CC polypeptides, to modulate biological activities of cells expressing PRO
CC polypeptides, and to detect the presence of mammalian lung, colon,
CC breast, prostate, rectal, cervical or liver tumours by comparing PRO
CC polypeptide expression in a cell sample to that in a control sample. Some
CC of the 275 sequences are also useful to stimulate the release of tumour
CC necrosis factor-alpha (TNF-alpha) from human blood, the proliferation or
CC differentiation of chondrocytes, the proliferation or gene expression in
CC pericyte cells, the release of proteoglycans from cartilage, the
CC proliferation of inner ear utricular supporting cells or of T-
CC lymphocytes, the release of a cytokine from peripheral blood monocytes
CC (PBMCs), or the proliferation of endothelial cells. Some of the PRO
CC polypeptides may modulate glucose or free fatty acid uptake by skeletal
CC muscle cells or by adipocytes; or inhibit binding of A-peptide to factor
CC VIIA. The PRO polypeptides can be used in assays to identify molecules
CC involved in binding interactions. The polynucleotides encoding PRO
CC polypeptides can be used to generate probes, antisense RNA/DNA,
CC transgenic or knock out animals and can be used in gene therapy
XX
SQ Sequence 586 AA;

Query Match 92.5%; Score 2815; DB 4; Length 586;
Best Local Similarity 100.0%; Pred. No. 1.2e-222;
Matches 549; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MALEIHMSDPMCLIENFNEQLKVNQEALEILSAITQPVVVVAIVGLYRTGKSYLMNKLAG 60
Db 1 MALEIHMSDPMCLIENFNEQLKVNQEALEILSAITQPVVVVAIVGLYRTGKSYLMNKLAG 60

Qy 61 KNKGFSVASTVQSHTKGIWIWCVPHPNWPNHTLVLLDTEGLGDVEKADNKNDIQIFALAL 120
Db 61 KNKGFSVASTVQSHTKGIWIWCVPHPNWPNHTLVLLDTEGLGDVEKADNKNDIQIFALAL 120

Qy 121 LLSSTFVYNTVNKIDQGAIDLLHNVTELTDLLKARNSPDLDRVEDPADSASFFPDLVWTL 180
Db 121 LLSSTFVYNTVNKIDQGAIDLLHNVTELTDLLKARNSPDLDRVEDPADSASFFPDLVWTL 180

Qy 181 RDFCLGLEIDGQLVTPDEYLENSLRPKQGSDQRVQNFNLPRLCIQKFFPKKKCFIFDLPA 240
Db 181 RDFCLGLEIDGQLVTPDEYLENSLRPKQGSDQRVQNFNLPRLCIQKFFPKKKCFIFDLPA 240

Qy 241 HQKKLAQLETLPDDELEPEFVQQVTEFCSYIFSHSMTKTLPGGIMVNGSRLKNLVLTYVN 300
Db 241 HQKKLAQLETLPDDELEPEFVQQVTEFCSYIFSHSMTKTLPGGIMVNGSRLKNLVLTYVN 300

Qy 301 AISSGDLPCIENAVLALAQRENSAAVQKAIAHYDQQMGQKVQLPMETLQELLDLHRTSER 360
Db 301 AISSGDLPCIENAVLALAQRENSAAVQKAIAHYDQQMGQKVQLPMETLQELLDLHRTSER 360

Qy 361 EAIEVFMKNSFKDVDQSFQKELETLLDAKQNDICKRNLEASSDYCSALLKDIFGPLEEAV 420
Db 361 EAIEVFMKNSFKDVDQSFQKELETLLDAKQNDICKRNLEASSDYCSALLKDIFGPLEEAV 420

Qy 421 KQGIYSKPGGHNLFIQKTEELKAKYYREPRKGIQAEEVLQKYLKSKESVSHAILQTDQAL 480
Db 421 KQGIYSKPGGHNLFIQKTEELKAKYYREPRKGIQAEEVLQKYLKSKESVSHAILQTDQAL 480

Qy 481 TETEKKKKEAQVKAEAEKAEAQRLAAIQRQNEQMMQERERLHQEQVRQMEIAKQNWLAEQ 540
Db 481 TETEKKKKEAQVKAEAEKAEAQRLAAIQRQNEQMMQERERLHQEQVRQMEIAKQNWLAEQ 540

Qy 541 QKMQEQQMQ 549
Db 541 QKMQEQQMQ 549

RESULT 3
ABB77445
ID ABB77445 standard; protein; 586 AA.
XX
AC ABB77445;
XX
DT 19-JUL-2002 (first entry)
XX
DE Human tumour marker protein GBP-TA.
XX
KW Human; tumour; cytostatic; cutaneous T cell lymphoma; CTCL; vaccine;
KW antigen-presenting cell; tumour-specific T cell.
XX
OS Homo sapiens.
XX
PN WO200238803-A2.
XX
PD 16-MAY-2002.
XX
PF 08-NOV-2001; 2001WO-DE004229.
XX
PR 08-NOV-2000; 2000DE-01055285.
XX
PA (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.
XX
PI Eichmueller S, Schadendorf D, Usener D;
XX
DR WPI; 2002-426959/45.
DR N-PSDB; ABL58973.
XX
PT Composition containing tumor-associated nucleic acid, useful for
PT diagnosis and treatment of tumors, especially cutaneous T cell lymphoma,
PT also derived proteins and antibodies.
XX
PS Claim 5; Fig 23; 84pp; German.
XX
CC The invention relates to a diagnostic composition containing at least one
CC of 23 nucleotide sequences (I, ABL58901-ABL58950) with altered expression
CC associated with tumours. (I), including antisense sequences and
CC ribozymes, also proteins (II, ABB77424-ABB77445) encoded by them and
CC antibodies specific for (II), are useful for diagnosis, monitoring and
CC treatment of tumours, especially cutaneous T cell lymphoma (CTCL). (II)
CC and antibodies to (II) are useful for vaccination. (II) can also be used
CC to prepare pre-loaded antigen-presenting cells or tumour-specific T cells
XX
SQ Sequence 586 AA;

Query Match 92.5%; Score 2815; DB 5; Length 586;
Best Local Similarity 100.0%; Pred. No. 1.2e-222;
Matches 549; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MALEIHMSDPMCLIENFNEQLKVNQEALEILSAITQPVVVVAIVGLYRTGKSYLMNKLAG 60
Db 1 MALEIHMSDPMCLIENFNEQLKVNQEALEILSAITQPVVVVAIVGLYRTGKSYLMNKLAG 60

Qy 61 KNKGFSVASTVQSHTKGIWIWCVPHPNWPNHTLVLLDTEGLGDVEKADNKNDIQIFALAL 120
Db 61 KNKGFSVASTVQSHTKGIWIWCVPHPNWPNHTLVLLDTEGLGDVEKADNKNDIQIFALAL 120

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Qy        121 LLSSTFVYNTVNKIDQGAIDLLHNVTELTDLLKARNSPDLDRVEDPADSASFFPDLVWTL 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 LLSSTFVYNTVNKIDQGAIDLLHNVTELTDLLKARNSPDLDRVEDPADSASFFPDLVWTL 180

Qy        181 RDFCLGLEIDGQLVTPDEYLENSLRPKQGSDQRVQNFNLPRLCIQKFFPKKKCFIFDLPA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 RDFCLGLEIDGQLVTPDEYLENSLRPKQGSDQRVQNFNLPRLCIQKFFPKKKCFIFDLPA 240

Qy        241 HQKKLAQLETLPDDELEPEFVQQVTEFCSYIFSHSMTKTLPGGIMVNGSRLKNLVLTYVN 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 HQKKLAQLETLPDDELEPEFVQQVTEFCSYIFSHSMTKTLPGGIMVNGSRLKNLVLTYVN 300

Qy        301 AISSGDLPCIENAVLALAQRENSAAVQKAIAHYDQQMGQKVQLPMETLQELLDLHRTSER 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 AISSGDLPCIENAVLALAQRENSAAVQKAIAHYDQQMGQKVQLPMETLQELLDLHRTSER 360

Qy        361 EAIEVFMKNSFKDVDQSFQKELETLLDAKQNDICKRNLEASSDYCSALLKDIFGPLEEAV 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 EAIEVFMKNSFKDVDQSFQKELETLLDAKQNDICKRNLEASSDYCSALLKDIFGPLEEAV 420

Qy        421 KQGIYSKPGGHNLFIQKTEELKAKYYREPRKGIQAEEVLQKYLKSKESVSHAILQTDQAL 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 KQGIYSKPGGHNLFIQKTEELKAKYYREPRKGIQAEEVLQKYLKSKESVSHAILQTDQAL 480

Qy        481 TETEKKKKEAQVKAEAEKAEAQRLAAIQRQNEQMMQERERLHQEQVRQMEIAKQNWLAEQ 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 TETEKKKKEAQVKAEAEKAEAQRLAAIQRQNEQMMQERERLHQEQVRQMEIAKQNWLAEQ 540

Qy        541 QKMQEQQMQ 549
              |||||||||
Db        541 QKMQEQQMQ 549
```

RESULT 4
ABO17638
ID ABO17638 standard; protein; 586 AA.
XX
AC ABO17638;
XX
DT 26-AUG-2003 (first entry)
XX
DE Novel human secreted and transmembrane protein PRO4987.
XX
KW Human; secreted and transmembrane protein; PRO; antiinflammatory;
KW antiarteriosclerotic; cardiant; anti-infertility; anti-HIV; cytostatic;
KW antidiabetic; gene therapy; tumour necrosis factor (TNF)-alpha release;
KW TNF-alpha release; cell proliferation; cell differentiation;
KW gene expression modulator; proteoglycan release; cytokine release;
KW tumour; inflammatory disease; organ failure; atherosclerosis;
KW cardiac injury; infertility; birth defect; premature aging; AIDS;
KW acquired immunodeficiency syndrome; cancer; diabetic complication;
KW chromosome mapping; gene mapping; pharmaceutical; diagnostic; biosensor;
KW bioreactor; tissue typing.
XX
OS Homo sapiens.
XX
PN US2003032156-A1.
XX
PD 13-FEB-2003.
XX
PF 06-MAY-2002; 2002US-00140474.
XX
PR 31-MAR-1997; 97WO-US005230.
PR 12-JUN-1998; 98WO-US012456.
PR 14-JUL-1998; 98WO-US014552.
PR 28-AUG-1998; 98WO-US017888.
PR 10-SEP-1998; 98WO-US018824.
PR 14-SEP-1998; 98WO-US019093.
PR 14-SEP-1998; 98WO-US019094.
PR 14-SEP-1998; 98WO-US019177.
PR 16-SEP-1998; 98WO-US019330.
PR 17-SEP-1998; 98WO-US019437.
PR 07-OCT-1998; 98WO-US021141.
PR 29-OCT-1998; 98WO-US022991.
PR 29-OCT-1998; 98WO-US022992.
PR 20-NOV-1998; 98WO-US024855.
PR 01-DEC-1998; 98WO-US025108.
PR 05-JAN-1999; 99WO-US000106.
PR 08-MAR-1999; 99WO-US005028.
PR 10-MAR-1999; 99WO-US005190.
PR 20-APR-1999; 99WO-US008615.
PR 14-MAY-1999; 99WO-US010733.
PR 02-JUN-1999; 99WO-US012252.
PR 01-SEP-1999; 99WO-US020111.
PR 08-SEP-1999; 99WO-US020594.
PR 13-SEP-1999; 99WO-US020944.
PR 15-SEP-1999; 99WO-US021090.
PR 15-SEP-1999; 99WO-US021547.
PR 05-OCT-1999; 99WO-US023089.
PR 29-NOV-1999; 99WO-US028214.
PR 30-NOV-1999; 99WO-US028313.
PR 30-NOV-1999; 99WO-US028409.
PR 01-DEC-1999; 99WO-US028301.
PR 01-DEC-1999; 99WO-US028634.
PR 02-DEC-1999; 99WO-US028551.
PR 02-DEC-1999; 99WO-US028564.
PR 02-DEC-1999; 99WO-US028565.
PR 16-DEC-1999; 99WO-US030095.
PR 20-DEC-1999; 99WO-US030911.
PR 20-DEC-1999; 99WO-US030999.
PR 22-DEC-1999; 99WO-US030720.
PR 30-DEC-1999; 99WO-US031243.
PR 30-DEC-1999; 99WO-US031274.
PR 05-JAN-2000; 2000WO-US000219.
PR 06-JAN-2000; 2000WO-US000277.
PR 06-JAN-2000; 2000WO-US000376.
PR 11-FEB-2000; 2000WO-US003565.
PR 18-FEB-2000; 2000WO-US004341.
PR 18-FEB-2000; 2000WO-US004342.
PR 22-FEB-2000; 2000WO-US004414.
PR 24-FEB-2000; 2000WO-US004914.
PR 24-FEB-2000; 2000WO-US005004.
PR 01-MAR-2000; 2000WO-US005601.
PR 02-MAR-2000; 2000WO-US005746.
PR 02-MAR-2000; 2000WO-US005841.
PR 10-MAR-2000; 2000WO-US006319.
PR 15-MAR-2000; 2000WO-US006884.
PR 20-MAR-2000; 2000WO-US007377.
PR 21-MAR-2000; 2000WO-US007532.
PR 30-MAR-2000; 2000WO-US008439.
PR 17-MAY-2000; 2000WO-US013705.
PR 22-MAY-2000; 2000WO-US014042.
PR 30-MAY-2000; 2000WO-US014941.
PR 02-JUN-2000; 2000WO-US015264.
PR 28-JUL-2000; 2000WO-US020710.
PR 11-AUG-2000; 2000WO-US022031.
PR 23-AUG-2000; 2000WO-US023522.
PR 24-AUG-2000; 2000WO-US023328.
PR 08-NOV-2000; 2000WO-US030952.
PR 10-NOV-2000; 2000WO-US030873.
PR 01-DEC-2000; 2000WO-US032678.
PR 20-DEC-2000; 2000US-00747259.
PR 20-DEC-2000; 2000WO-US034956.
PR 28-FEB-2001; 2001US-00796498.
PR 28-FEB-2001; 2001WO-US006520.
PR 01-MAR-2001; 2001WO-US006666.
PR 09-MAR-2001; 2001US-00802706.
PR 14-MAR-2001; 2001US-00808689.
PR 22-MAR-2001; 2001US-00816744.
PR 05-APR-2001; 2001US-00828366.
PR 10-MAY-2001; 2001US-00854208.
PR 10-MAY-2001; 2001US-00854280.
PR 18-MAY-2001; 2001US-00860216.
PR 25-MAY-2001; 2001US-00866028.
PR 25-MAY-2001; 2001US-00866034.

PR 25-MAY-2001; 2001WO-US017092.
PR 01-JUN-2001; 2001US-00872035.
PR 01-JUN-2001; 2001WO-US017800.
PR 05-JUN-2001; 2001US-00874503.
PR 14-JUN-2001; 2001US-00882636.
PR 19-JUN-2001; 2001US-00886342.
PR 20-JUN-2001; 2001WO-US019692.
PR 21-JUN-2001; 2001US-00887879.
PR 22-JUN-2001; 2001WO-US020116.
PR 29-JUN-2001; 2001WO-US021066.
PR 09-JUL-2001; 2001WO-US021735.
PR 18-JUL-2001; 2001US-00908827.
PR 06-AUG-2001; 2001US-00924419.
PR 09-AUG-2001; 2001US-00927796.
PR 16-AUG-2001; 2001US-00931836.
PR 19-DEC-2001; 2001US-00028072.
XX
PA (GETH) GENENTECH INC.
XX
PI Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, Gao W;
PI Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;
PI Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;
XX
DR WPI; 2003-341980/32.
DR N-PSDB; ACD23875.
XX
PT New secreted and transmembrane PRO nucleic acids, for treating
PT inflammation, organ failure, atherosclerosis, cardiac injury,
PT infertility, birth defects, premature aging, axquired immunodeficiency
PT syndrome (AIDS), or cancer.
XX
PS Claim 12; Fig 46; 660pp; English.
XX
CC The invention describes an isolated nucleic acid (I) comprising, or which
CC has 80 % sequence identity to, or the full-length coding sequence of, one
CC of 275 nucleotide sequences, and which encodes a corresponding
CC polypeptide selected from 275 amino acid sequences, where all sequences
CC are given in the specification. The polypeptide encoded by (I) is used to
CC detect PRO polypeptides, link a bioactive molecule to a cell expressing a
CC PRO polypeptide, modulate a biological activity of a cell, stimulate the
CC release of tumour necrosis factor (TNF)-alpha from human blood, modulate
CC the uptake of glucose or free fatty acid by cells, stimulate or inhibit
CC the proliferation or differentiation of cells or gene expression,
CC stimulate the release of proteoglycans, stimulate the release of cytokine
CC from peripheral blood mononuclear cells, inhibit the binding of A-peptide
CC to factor VIIA, or detect the presence of tumour in a mammal. The nucleic
CC acid and polypeptide encoded by it, are useful for treating inflammatory
CC diseases, organ failure, atherosclerosis, cardiac injury, infertility,
CC birth defects, premature aging, acquired immunodeficiency syndrome
CC (AIDS), cancer, or diabetic complications. The nucleic acid is useful as
CC hybridisation probes, in chromosome and gene mapping, and in generating
CC antisense RNA or DNA. The polypeptides are useful as pharmaceuticals,
CC diagnostics, biosensors or bioreactors. Both are useful in tissue typing.
CC This is the amino acid sequence of a novel human secreted and
CC transmembrane PRO polypeptide
XX
SQ Sequence 586 AA;

Query Match 92.5%; Score 2815; DB 6; Length 586;
Best Local Similarity 100.0%; Pred. No. 1.2e-222;
Matches 549; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 MALEIHMSDPMCLIENFNEQLKVNQEALEILSAITQPVVVVAIVGLYRTGKSYLMNKLAG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MALEIHMSDPMCLIENFNEQLKVNQEALEILSAITQPVVVVAIVGLYRTGKSYLMNKLAG 60

Qy         61 KNKGFSVASTVQSHTKGIWIWCVPHPNWPNHTLVLLDTEGLGDVEKADNKNDIQIFALAL 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 KNKGFSVASTVQSHTKGIWIWCVPHPNWPNHTLVLLDTEGLGDVEKADNKNDIQIFALAL 120

Qy        121 LLSSTFVYNTVNKIDQGAIDLLHNVTELTDLLKARNSPDLDRVEDPADSASFFPDLVWTL 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 LLSSTFVYNTVNKIDQGAIDLLHNVTELTDLLKARNSPDLDRVEDPADSASFFPDLVWTL 180

Qy        181 RDFCLGLEIDGQLVTPDEYLENSLRPKQGSDQRVQNFNLPRLCIQKFFPKKKCFIFDLPA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 RDFCLGLEIDGQLVTPDEYLENSLRPKQGSDQRVQNFNLPRLCIQKFFPKKKCFIFDLPA 240

Qy        241 HQKKLAQLETLPDDELEPEFVQQVTEFCSYIFSHSMTKTLPGGIMVNGSRLKNLVLTYVN 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 HQKKLAQLETLPDDELEPEFVQQVTEFCSYIFSHSMTKTLPGGIMVNGSRLKNLVLTYVN 300

Qy        301 AISSGDLPCIENAVLALAQRENSAAVQKAIAHYDQQMGQKVQLPMETLQELLDLHRTSER 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 AISSGDLPCIENAVLALAQRENSAAVQKAIAHYDQQMGQKVQLPMETLQELLDLHRTSER 360

Qy        361 EAIEVFMKNSFKDVDQSFQKELETLLDAKQNDICKRNLEASSDYCSALLKDIFGPLEEAV 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 EAIEVFMKNSFKDVDQSFQKELETLLDAKQNDICKRNLEASSDYCSALLKDIFGPLEEAV 420

Qy        421 KQGIYSKPGGHNLFIQKTEELKAKYYREPRKGIQAEEVLQKYLKSKESVSHAILQTDQAL 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 KQGIYSKPGGHNLFIQKTEELKAKYYREPRKGIQAEEVLQKYLKSKESVSHAILQTDQAL 480

Qy        481 TETEKKKKEAQVKAEAEKAEAQRLAAIQRQNEQMMQERERLHQEQVRQMEIAKQNWLAEQ 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 TETEKKKKEAQVKAEAEKAEAQRLAAIQRQNEQMMQERERLHQEQVRQMEIAKQNWLAEQ 540

Qy        541 QKMQEQQMQ 549
              |||||||||
Db        541 QKMQEQQMQ 549
```

RESULT 5
ABU80892
ID ABU80892 standard; protein; 586 AA.
XX
AC ABU80892;
XX
DT 23-JUN-2003 (first entry)
XX
DE Human PRO polypeptide #23.
XX
KW Human; PRO polypeptide; secreted and transmembrane protein;
KW anti-PRO antibody; diagnostic assay; gene expression; diabetes;
KW bone disorder; cartilage disorder; rheumatoid arthritis; obesity;
KW sports injury; osteoarthritis; hyper-insulinaemia; hypo-insulinaemia;
KW hearing loss; coagulation disorder; stroke; heart attack; cardiant;
KW antidiabetic; anorectic; vulnerary; antiarthritic; osteopathic;
KW antirheumatic; auditory; cerebroprotective; angiogenic.
XX
OS Homo sapiens.
XX
PN US2003004311-A1.
XX
PD 02-JAN-2003.
XX
PF 19-DEC-2001; 2001US-00028072.
XX
PR 18-JUN-1997; 97US-0049911P.
PR 26-AUG-1997; 97US-0056974P.
PR 17-SEP-1997; 97US-0059113P.
PR 17-SEP-1997; 97US-0059115P.
PR 17-SEP-1997; 97US-0059117P.
PR 17-SEP-1997; 97US-0059122P.
PR 17-SEP-1997; 97US-0059184P.
PR 18-SEP-1997; 97US-0059263P.
PR 19-SEP-1997; 97US-0059352P.
PR 19-SEP-1997; 97US-0059588P.
PR 24-SEP-1997; 97US-0059836P.
PR 17-OCT-1997; 97US-0062250P.
PR 17-OCT-1997; 97US-0062285P.
PR 17-OCT-1997; 97US-0062287P.
PR 17-OCT-1997; 97US-0063755P.
PR 24-OCT-1997; 97US-0062814P.
PR 24-OCT-1997; 97US-0062816P.

PR 24-OCT-1997; 97US-0063045P.
PR 24-OCT-1997; 97US-0063082P.
PR 24-OCT-1997; 97US-0063127P.
PR 27-OCT-1997; 97US-0063327P.
PR 27-OCT-1997; 97US-0063329P.
PR 28-OCT-1997; 97US-0063550P.
PR 28-OCT-1997; 97US-0063561P.
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PR 29-OCT-1997; 97US-0063733P.
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PR 03-NOV-1997; 97US-0064248P.
PR 07-NOV-1997; 97US-0064809P.
PR 12-NOV-1997; 97US-0065186P.
PR 17-NOV-1997; 97US-0065846P.
PR 21-NOV-1997; 97US-0066364P.
PR 24-NOV-1997; 97US-0066453P.
PR 24-NOV-1997; 97US-0066511P.
PR 24-NOV-1997; 97US-0066770P.
PR 11-DEC-1997; 97US-0069212P.
PR 11-DEC-1997; 97US-0069278P.
PR 11-DEC-1997; 97US-0069334P.
PR 16-DEC-1997; 97US-0069694P.
PR 23-JAN-1998; 98US-0072320P.
PR 04-FEB-1998; 98US-0073612P.
PR 09-FEB-1998; 98US-0074086P.
PR 09-FEB-1998; 98US-0074092P.
PR 12-MAR-1998; 98US-0077791P.
PR 20-MAR-1998; 98US-0078910P.
PR 25-MAR-1998; 98US-0079294P.
PR 27-MAR-1998; 98US-0079663P.
PR 27-MAR-1998; 98US-0079728P.
PR 31-MAR-1998; 98US-0080165P.
PR 12-JUN-1998; 98WO-US012456.
PR 14-JUL-1998; 98WO-US014552.
PR 28-AUG-1998; 98WO-US017888.
PR 10-SEP-1998; 98WO-US018824.
PR 14-SEP-1998; 98WO-US019093.
PR 14-SEP-1998; 98WO-US019094.
PR 14-SEP-1998; 98WO-US019177.
PR 16-SEP-1998; 98WO-US019330.
PR 17-SEP-1998; 98WO-US019437.
PR 07-OCT-1998; 98WO-US021141.
PR 29-OCT-1998; 98WO-US022991.
PR 29-OCT-1998; 98WO-US022992.
PR 20-NOV-1998; 98WO-US024855.
PR 01-DEC-1998; 98WO-US025108.
PR 05-JAN-1999; 99WO-US000106.
PR 08-MAR-1999; 99WO-US005028.
PR 10-MAR-1999; 99WO-US005190.
PR 20-APR-1999; 99WO-US008615.
PR 14-MAY-1999; 99WO-US010733.
PR 02-JUN-1999; 99WO-US012252.
PR 01-SEP-1999; 99WO-US020111.
PR 08-SEP-1999; 99WO-US020594.
PR 13-SEP-1999; 99WO-US020944.
PR 15-SEP-1999; 99WO-US021090.
PR 15-SEP-1999; 99WO-US021547.
PR 05-OCT-1999; 99WO-US023089.
PR 29-NOV-1999; 99WO-US028214.
PR 30-NOV-1999; 99WO-US028313.
PR 30-NOV-1999; 99WO-US028409.
PR 01-DEC-1999; 99WO-US028301.
PR 01-DEC-1999; 99WO-US028634.
PR 02-DEC-1999; 99WO-US028551.
PR 02-DEC-1999; 99WO-US028564.
PR 02-DEC-1999; 99WO-US028565.
PR 16-DEC-1999; 99WO-US030095.
PR 20-DEC-1999; 99WO-US030911.
PR 20-DEC-1999; 99WO-US030999.
PR 30-DEC-1999; 99WO-US031243.
PR 30-DEC-1999; 99WO-US031274.
PR 05-JAN-2000; 2000WO-US000219.
PR 06-JAN-2000; 2000WO-US000277.
PR 06-JAN-2000; 2000WO-US000376.
PR 11-FEB-2000; 2000WO-US003565.
PR 18-FEB-2000; 2000WO-US004341.
PR 18-FEB-2000; 2000WO-US004342.
PR 22-FEB-2000; 2000WO-US004414.
PR 24-FEB-2000; 2000WO-US004914.
PR 24-FEB-2000; 2000WO-US005004.
PR 01-MAR-2000; 2000WO-US005601.
PR 02-MAR-2000; 2000WO-US005746.
XX
PA (GETH) GENENTECH INC.
XX
PI Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, Gao W;
PI Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;
PI Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;
XX
DR WPI; 2003-352836/33.
DR N-PSDB; ACA67016.
XX
PT New isolated PRO polypeptide useful for treating diabetes, rheumatoid
PT arthritis, sports injuries, obesity, hearing loss in mammals, stroke, or
PT heart attack.
XX
PS Claim 12; Fig 46; 643pp; English.
XX
CC The present invention relates to the isolation of novel human PRO
CC polypeptides, and the polynucleotide sequences encoding them. The PRO
CC polypeptides are secreted and transmembrane proteins. The PRO
CC polypeptides and polynucleotides are useful for preparing a medicament
CC useful in the treatment of diabetes, bone and/or cartilage disorders
CC (e.g. rheumatoid arthritis, sports injuries, osteoarthritis), obesity,
CC hyper- or hypo-insulinaemia, hearing loss, and coagulation disorders
CC (e.g. stroke, heart attack). Anti-PRO antibodies are useful in diagnostic
CC assays for PRO, by detecting its expression in specific cells, tissues or
CC serum, and for affinity purification of PRO from recombinant cell culture
CC or natural sources. ABU80870-ABU81144 represent the human PRO
CC polypeptides of the invention. Note: The sequence data for this patent
CC was obtained in electronic format directly from the USPTO web site at
CC seqdata.uspto.gov/psipsDIDEntry.html
XX
SQ Sequence 586 AA;

Query Match 92.5%; Score 2815; DB 6; Length 586;
Best Local Similarity 100.0%; Pred. No. 1.2e-222;
Matches 549; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 MALEIHMSDPMCLIENFNEQLKVNQEALEILSAITQPVVVVAIVGLYRTGKSYLMNKLAG 60
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Db          1 MALEIHMSDPMCLIENFNEQLKVNQEALEILSAITQPVVVVAIVGLYRTGKSYLMNKLAG 60

Qy         61 KNKGFSVASTVQSHTKGIWIWCVPHPNWPNHTLVLLDTEGLGDVEKADNKNDIQIFALAL 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 KNKGFSVASTVQSHTKGIWIWCVPHPNWPNHTLVLLDTEGLGDVEKADNKNDIQIFALAL 120

Qy        121 LLSSTFVYNTVNKIDQGAIDLLHNVTELTDLLKARNSPDLDRVEDPADSASFFPDLVWTL 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 LLSSTFVYNTVNKIDQGAIDLLHNVTELTDLLKARNSPDLDRVEDPADSASFFPDLVWTL 180

Qy        181 RDFCLGLEIDGQLVTPDEYLENSLRPKQGSDQRVQNFNLPRLCIQKFFPKKKCFIFDLPA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 RDFCLGLEIDGQLVTPDEYLENSLRPKQGSDQRVQNFNLPRLCIQKFFPKKKCFIFDLPA 240

Qy        241 HQKKLAQLETLPDDELEPEFVQQVTEFCSYIFSHSMTKTLPGGIMVNGSRLKNLVLTYVN 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 HQKKLAQLETLPDDELEPEFVQQVTEFCSYIFSHSMTKTLPGGIMVNGSRLKNLVLTYVN 300

Qy        301 AISSGDLPCIENAVLALAQRENSAAVQKAIAHYDQQMGQKVQLPMETLQELLDLHRTSER 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 AISSGDLPCIENAVLALAQRENSAAVQKAIAHYDQQMGQKVQLPMETLQELLDLHRTSER 360

Qy        361 EAIEVFMKNSFKDVDQSFQKELETLLDAKQNDICKRNLEASSDYCSALLKDIFGPLEEAV 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

```
Db        361 EAIEVFMKNSFKDVDQSFQKELETLLDAKQNDICKRNLEASSDYCSALLKDIFGPLEEAV 420

Qy        421 KQGIYSKPGGHNLFIQKTEELKAKYYREPRKGIQAEEVLQKYLKSKESVSHAILQTDQAL 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 KQGIYSKPGGHNLFIQKTEELKAKYYREPRKGIQAEEVLQKYLKSKESVSHAILQTDQAL 480

Qy        481 TETEKKKKEAQVKAEAEKAEAQRLAAIQRQNEQMMQERERLHQEQVRQMEIAKQNWLAEQ 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 TETEKKKKEAQVKAEAEKAEAQRLAAIQRQNEQMMQERERLHQEQVRQMEIAKQNWLAEQ 540

Qy        541 QKMQEQQMQ 549
              |||||||||
Db        541 QKMQEQQMQ 549
```

RESULT 6
ABU66592
ID ABU66592 standard; protein; 586 AA.
XX
AC ABU66592;
XX
DT 23-MAY-2003 (first entry)
XX
DE Human PRO polypeptide #23.
XX
KW Human; PRO polypeptide; secreted and transmembrane protein;
KW tumour necrosis factor-alpha; TNF-alpha; blood; proliferation;
KW differentiation; chondrocyte; tumour; genetic disorder; cytostatic.
XX
OS Homo sapiens.
XX
PN US2003036180-A1.
XX
PD 20-FEB-2003.
XX
PF 09-MAY-2002; 2002US-00143114.
XX
PR 31-MAR-1997; 97WO-US005230.
PR 12-JUN-1998; 98WO-US012456.
PR 14-JUL-1998; 98WO-US014552.
PR 28-AUG-1998; 98WO-US017888.
PR 10-SEP-1998; 98WO-US018824.
PR 14-SEP-1998; 98WO-US019093.
PR 14-SEP-1998; 98WO-US019094.
PR 14-SEP-1998; 98WO-US019177.
PR 16-SEP-1998; 98WO-US019330.
PR 17-SEP-1998; 98WO-US019437.
PR 07-OCT-1998; 98WO-US021141.
PR 29-OCT-1998; 98WO-US022991.
PR 29-OCT-1998; 98WO-US022992.
PR 20-NOV-1998; 98WO-US024855.
PR 01-DEC-1998; 98WO-US025108.
PR 05-JAN-1999; 99WO-US000106.
PR 08-MAR-1999; 99WO-US005028.
PR 10-MAR-1999; 99WO-US005190.
PR 20-APR-1999; 99WO-US008615.
PR 14-MAY-1999; 99WO-US010733.
PR 02-JUN-1999; 99WO-US012252.
PR 01-SEP-1999; 99WO-US020111.
PR 08-SEP-1999; 99WO-US020594.
PR 13-SEP-1999; 99WO-US020944.
PR 15-SEP-1999; 99WO-US021090.
PR 15-SEP-1999; 99WO-US021547.
PR 05-OCT-1999; 99WO-US023089.
PR 29-NOV-1999; 99WO-US028214.
PR 30-NOV-1999; 99WO-US028313.
PR 30-NOV-1999; 99WO-US028409.
PR 01-DEC-1999; 99WO-US028301.
PR 01-DEC-1999; 99WO-US028634.
PR 02-DEC-1999; 99WO-US028551.
PR 02-DEC-1999; 99WO-US028564.
PR 02-DEC-1999; 99WO-US028565.
PR 16-DEC-1999; 99WO-US030095.
PR 20-DEC-1999; 99WO-US030911.
PR 20-DEC-1999; 99WO-US030999.
PR 22-DEC-1999; 99WO-US030720.
PR 30-DEC-1999; 99WO-US031243.
PR 30-DEC-1999; 99WO-US031274.
PR 05-JAN-2000; 2000WO-US000219.
PR 06-JAN-2000; 2000WO-US000277.
PR 06-JAN-2000; 2000WO-US000376.
PR 11-FEB-2000; 2000WO-US003565.
PR 18-FEB-2000; 2000WO-US004341.
PR 18-FEB-2000; 2000WO-US004342.
PR 22-FEB-2000; 2000WO-US004414.
PR 24-FEB-2000; 2000WO-US004914.
PR 24-FEB-2000; 2000WO-US005004.
PR 01-MAR-2000; 2000WO-US005601.
PR 02-MAR-2000; 2000WO-US005746.
PR 02-MAR-2000; 2000WO-US005841.
PR 10-MAR-2000; 2000WO-US006319.
PR 15-MAR-2000; 2000WO-US006884.
PR 20-MAR-2000; 2000WO-US007377.
PR 21-MAR-2000; 2000WO-US007532.
PR 30-MAR-2000; 2000WO-US008439.
PR 17-MAY-2000; 2000WO-US013705.
PR 22-MAY-2000; 2000WO-US014042.
PR 30-MAY-2000; 2000WO-US014941.
PR 02-JUN-2000; 2000WO-US015264.
PR 28-JUL-2000; 2000WO-US020710.
PR 11-AUG-2000; 2000WO-US022031.
PR 23-AUG-2000; 2000WO-US023522.
PR 24-AUG-2000; 2000WO-US023328.
PR 08-NOV-2000; 2000WO-US030952.
PR 10-NOV-2000; 2000WO-US030873.
PR 01-DEC-2000; 2000WO-US032678.
PR 20-DEC-2000; 2000US-00747259.
PR 20-DEC-2000; 2000WO-US034956.
PR 28-FEB-2001; 2001US-00796498.
PR 28-FEB-2001; 2001WO-US006520.
PR 01-MAR-2001; 2001WO-US006666.
PR 09-MAR-2001; 2001US-00802706.
PR 14-MAR-2001; 2001US-00808689.
PR 22-MAR-2001; 2001US-00816744.
PR 05-APR-2001; 2001US-00828366.
PR 10-MAY-2001; 2001US-00854208.
PR 10-MAY-2001; 2001US-00854280.
PR 18-MAY-2001; 2001US-00860216.
PR 25-MAY-2001; 2001US-00866028.
PR 25-MAY-2001; 2001US-00866034.
PR 25-MAY-2001; 2001WO-US017092.
PR 01-JUN-2001; 2001US-00872035.
PR 01-JUN-2001; 2001WO-US017800.
PR 05-JUN-2001; 2001US-00874503.
PR 14-JUN-2001; 2001US-00882636.
PR 19-JUN-2001; 2001US-00886342.
PR 20-JUN-2001; 2001WO-US019692.
PR 21-JUN-2001; 2001US-00887879.
PR 22-JUN-2001; 2001WO-US020116.
PR 29-JUN-2001; 2001WO-US021066.
PR 09-JUL-2001; 2001WO-US021735.
PR 18-JUL-2001; 2001US-00908827.
PR 06-AUG-2001; 2001US-00924419.
PR 09-AUG-2001; 2001US-00927796.
PR 16-AUG-2001; 2001US-00931836.
PR 19-DEC-2001; 2001US-00028072.
XX
PA (GETH) GENENTECH INC.
XX
PI Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, Gao W;
PI Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;
PI Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;
XX
DR WPI; 2003-332040/31.
DR N-PSDB; ACA03625.
XX

PT New secreted and transmembrane PRO nucleic acids, useful for gene
PT therapy, in chromosome and gene mapping, as chromosome markers, in tissue
PT typing, and in chromosome identification.
XX
PS Claim 12; Fig 46; 660pp; English.
XX
CC The present invention relates to the isolation of novel human PRO
CC polypeptides, and the polynucleotide sequences encoding them. The PRO
CC polypeptides are secreted and transmembrane proteins. The PRO
CC polypeptides are useful for detecting other PRO polypeptides, for linking
CC bioactive molecules to cells expressing PRO polypeptides, for modulating
CC biological activities of cells expressing PRO polypeptides, and for for
CC identifying agonists or antagonists. The PRO polypeptides are useful for
CC for stimulating the release of tumour necrosis factor (TNF)-alpha from
CC human blood, for stimulating the proliferation or differentiation of
CC chondrocytes, and detecting the presence of tumours. The polynucleotide
CC sequences encoding PRO polypeptides are useful as hybridisation probes,
CC in chromosome and gene mapping, in the generation of antisense RNA and
CC DNA, in the preparation of PRO polypeptides, for generating transgenic
CC animals or knockout animals, for the genetic analysis of individuals with
CC genetic disorders, and in gene therapy. ABU66570-ABU66844 represent the
CC human PRO polypeptides of the invention. Note: The sequence data for this
CC patent was obtained in electronic format directly from the USPTO web site
CC at seqdata.uspto.gov/psipsDIDEntry.html
XX
SQ Sequence 586 AA;

Query Match 92.5%; Score 2815; DB 6; Length 586;
Best Local Similarity 100.0%; Pred. No. 1.2e-222;
Matches 549; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 MALEIHMSDPMCLIENFNEQLKVNQEALEILSAITQPVVVVAIVGLYRTGKSYLMNKLAG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MALEIHMSDPMCLIENFNEQLKVNQEALEILSAITQPVVVVAIVGLYRTGKSYLMNKLAG 60

Qy         61 KNKGFSVASTVQSHTKGIWIWCVPHPNWPNHTLVLLDTEGLGDVEKADNKNDIQIFALAL 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 KNKGFSVASTVQSHTKGIWIWCVPHPNWPNHTLVLLDTEGLGDVEKADNKNDIQIFALAL 120

Qy        121 LLSSTFVYNTVNKIDQGAIDLLHNVTELTDLLKARNSPDLDRVEDPADSASFFPDLVWTL 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 LLSSTFVYNTVNKIDQGAIDLLHNVTELTDLLKARNSPDLDRVEDPADSASFFPDLVWTL 180

Qy        181 RDFCLGLEIDGQLVTPDEYLENSLRPKQGSDQRVQNFNLPRLCIQKFFPKKKCFIFDLPA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 RDFCLGLEIDGQLVTPDEYLENSLRPKQGSDQRVQNFNLPRLCIQKFFPKKKCFIFDLPA 240

Qy        241 HQKKLAQLETLPDDELEPEFVQQVTEFCSYIFSHSMTKTLPGGIMVNGSRLKNLVLTYVN 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 HQKKLAQLETLPDDELEPEFVQQVTEFCSYIFSHSMTKTLPGGIMVNGSRLKNLVLTYVN 300

Qy        301 AISSGDLPCIENAVLALAQRENSAAVQKAIAHYDQQMGQKVQLPMETLQELLDLHRTSER 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 AISSGDLPCIENAVLALAQRENSAAVQKAIAHYDQQMGQKVQLPMETLQELLDLHRTSER 360

Qy        361 EAIEVFMKNSFKDVDQSFQKELETLLDAKQNDICKRNLEASSDYCSALLKDIFGPLEEAV 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 EAIEVFMKNSFKDVDQSFQKELETLLDAKQNDICKRNLEASSDYCSALLKDIFGPLEEAV 420

Qy        421 KQGIYSKPGGHNLFIQKTEELKAKYYREPRKGIQAEEVLQKYLKSKESVSHAILQTDQAL 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 KQGIYSKPGGHNLFIQKTEELKAKYYREPRKGIQAEEVLQKYLKSKESVSHAILQTDQAL 480

Qy        481 TETEKKKKEAQVKAEAEKAEAQRLAAIQRQNEQMMQERERLHQEQVRQMEIAKQNWLAEQ 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 TETEKKKKEAQVKAEAEKAEAQRLAAIQRQNEQMMQERERLHQEQVRQMEIAKQNWLAEQ 540

Qy        541 QKMQEQQMQ 549
              |||||||||
Db        541 QKMQEQQMQ 549
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RESULT 7

ABU59673
ID ABU59673 standard; protein; 586 AA.
XX
AC ABU59673;
XX
DT 13-MAY-2003 (first entry)
XX
DE Novel secreted and transmembrane protein PRO4987.
XX
KW Human; PRO; hypertrophy of neonatal heart; angiogenesis; wound healing;
KW cardiac insufficiency disorder; cancer; tumour; immune response;
KW adrenal cortical capillary endothelial growth; c-fos induction;
KW vascular endothelial growth factor inhibition; VEGF inhibition;
KW endothelial cell growth inhibitor; T-lymphocytes stimulation;
KW retinal neurons cell survival; rod photoreceptor cell survival;
KW retinal disorder; retinitis pigmentosum; kidney disorder;
KW mammalian kidney mesangial cell proliferation; Berger disease;
KW dermatitis; herpetiformis; Crohn's disease; chondrocyte proliferation;
KW chondrocyte redifferentiation; sports injury; arthritis.
XX
OS Homo sapiens.
XX
PN US2003017563-A1.
XX
PD 23-JAN-2003.
XX
PF 07-MAY-2002; 2002US-00140808.
XX
PR 31-MAR-1997; 97WO-US005230.
PR 12-JUN-1998; 98WO-US012456.
PR 14-JUL-1998; 98WO-US014552.
PR 28-AUG-1998; 98WO-US017888.
PR 10-SEP-1998; 98WO-US018824.
PR 14-SEP-1998; 98WO-US019093.
PR 14-SEP-1998; 98WO-US019094.
PR 14-SEP-1998; 98WO-US019177.
PR 16-SEP-1998; 98WO-US019330.
PR 17-SEP-1998; 98WO-US019437.
PR 07-OCT-1998; 98WO-US021141.
PR 29-OCT-1998; 98WO-US022991.
PR 29-OCT-1998; 98WO-US022992.
PR 20-NOV-1998; 98WO-US024855.
PR 01-DEC-1998; 98WO-US025108.
PR 05-JAN-1999; 99WO-US000106.
PR 08-MAR-1999; 99WO-US005028.
PR 10-MAR-1999; 99WO-US005190.
PR 20-APR-1999; 99WO-US008615.
PR 14-MAY-1999; 99WO-US010733.
PR 02-JUN-1999; 99WO-US012252.
PR 01-SEP-1999; 99WO-US020111.
PR 08-SEP-1999; 99WO-US020594.
PR 13-SEP-1999; 99WO-US020944.
PR 15-SEP-1999; 99WO-US021090.
PR 15-SEP-1999; 99WO-US021547.
PR 05-OCT-1999; 99WO-US023089.
PR 29-NOV-1999; 99WO-US028214.
PR 30-NOV-1999; 99WO-US028313.
PR 30-NOV-1999; 99WO-US028409.
PR 01-DEC-1999; 99WO-US028301.
PR 01-DEC-1999; 99WO-US028634.
PR 02-DEC-1999; 99WO-US028551.
PR 02-DEC-1999; 99WO-US028564.
PR 02-DEC-1999; 99WO-US028565.
PR 16-DEC-1999; 99WO-US030095.
PR 20-DEC-1999; 99WO-US030911.
PR 20-DEC-1999; 99WO-US030999.
PR 22-DEC-1999; 99WO-US030720.
PR 30-DEC-1999; 99WO-US031243.
PR 30-DEC-1999; 99WO-US031274.
PR 05-JAN-2000; 2000WO-US000219.
PR 06-JAN-2000; 2000WO-US000277.
PR 06-JAN-2000; 2000WO-US000376.
PR 11-FEB-2000; 2000WO-US003565.

PR 18-FEB-2000; 2000WO-US004341.
PR 18-FEB-2000; 2000WO-US004342.
PR 22-FEB-2000; 2000WO-US004414.
PR 24-FEB-2000; 2000WO-US004914.
PR 24-FEB-2000; 2000WO-US005004.
PR 01-MAR-2000; 2000WO-US005601.
PR 02-MAR-2000; 2000WO-US005746.
PR 02-MAR-2000; 2000WO-US005841.
PR 10-MAR-2000; 2000WO-US006319.
PR 15-MAR-2000; 2000WO-US006884.
PR 20-MAR-2000; 2000WO-US007377.
PR 21-MAR-2000; 2000WO-US007532.
PR 30-MAR-2000; 2000WO-US008439.
PR 17-MAY-2000; 2000WO-US013705.
PR 22-MAY-2000; 2000WO-US014042.
PR 30-MAY-2000; 2000WO-US014941.
PR 02-JUN-2000; 2000WO-US015264.
PR 28-JUL-2000; 2000WO-US020710.
PR 11-AUG-2000; 2000WO-US022031.
PR 23-AUG-2000; 2000WO-US023522.
PR 24-AUG-2000; 2000WO-US023328.
PR 08-NOV-2000; 2000WO-US030952.
PR 10-NOV-2000; 2000WO-US030873.
PR 01-DEC-2000; 2000WO-US032678.
PR 20-DEC-2000; 2000US-00747259.
PR 20-DEC-2000; 2000WO-US034956.
PR 28-FEB-2001; 2001US-00796498.
PR 28-FEB-2001; 2001WO-US006520.
PR 01-MAR-2001; 2001WO-US006666.
PR 09-MAR-2001; 2001US-00802706.
PR 14-MAR-2001; 2001US-00808689.
PR 22-MAR-2001; 2001US-00816744.
PR 05-APR-2001; 2001US-00828366.
PR 10-MAY-2001; 2001US-00854208.
PR 10-MAY-2001; 2001US-00854280.
PR 18-MAY-2001; 2001US-00860216.
PR 25-MAY-2001; 2001US-00866028.
PR 25-MAY-2001; 2001US-00866034.
PR 25-MAY-2001; 2001WO-US017092.
PR 01-JUN-2001; 2001US-00872035.
PR 01-JUN-2001; 2001WO-US017800.
PR 05-JUN-2001; 2001US-00874503.
PR 14-JUN-2001; 2001US-00882636.
PR 19-JUN-2001; 2001US-00886342.
PR 20-JUN-2001; 2001WO-US019692.
PR 21-JUN-2001; 2001US-00887879.
PR 22-JUN-2001; 2001WO-US020116.
PR 29-JUN-2001; 2001WO-US021066.
PR 09-JUL-2001; 2001WO-US021735.
PR 18-JUL-2001; 2001US-00908827.
PR 06-AUG-2001; 2001US-00924419.
PR 09-AUG-2001; 2001US-00927796.
PR 16-AUG-2001; 2001US-00931836.
PR 19-DEC-2001; 2001US-00028072.
XX
PA (GETH) GENENTECH INC.
XX
PI Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, Gao W;
PI Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;
PI Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;
XX
DR WPI; 2003-148238/14.
DR N-PSDB; ABX89163.
XX
PT Two hundred and seventy five nucleic acids encoding PRO polypeptides,
PT useful for treating pericyte-associated tumors, diabetes and various bone
PT and/or cartilage disorders, e.g. arthritis.
XX
PS Claim 12; Fig 46; 659pp; English.
XX
CC The invention describes an isolated human PRO polypeptide. The PRO
CC polypeptides are useful in detecting PRO polypeptides in a sample, in
CC linking a bioactive molecule to a cell expressing a PRO polypeptide, and
CC in modulating at least one biological activity of a cell expressing a PRO
CC polypeptide. PRO1312 stimulates hypertrophy of neonatal heart and is thus
CC useful for treating cardiac insufficiency disorders. PRO1154 and PRO1186
CC stimulate adrenal cortical capillary endothelial growth, and PRO536,
CC PRO943, PRO828, PRO826, PRO1068 or PRO535, PRO826, PRO819, PRO1126,
CC PRO1360 and PRO1387 induce c-fos in endothelial cells, and are thus
CC useful for treating conditions or disorders where angiogenesis would be
CC beneficial, e.g. wound healing and antagonist of this polypeptide are
CC useful for treating cancerous tumours. PRO812 inhibits vascular
CC endothelial growth factor (VEGF) stimulated proliferation of endothelial
CC cells and is thus useful for inhibiting endothelial cell growth in
CC mammals which would be beneficial in inhibiting tumour growth. PRO826,
CC PRO1068, PRO1184, PRO1346 and PRO1375 stimulate proliferation of
CC stimulated T-lymphocytes and are therapeutically useful for enhancing
CC immune response. PRO828, PRO826, PRO1068 or PRO1132 enhance survival of
CC retinal neurons cells (PRO1132 is also enhances survival/proliferation of
CC rod photoreceptor cells) and therefore are useful for treating retinal
CC disorders of injuries, e.g. retinitis pigmentosum, AMD. PRO819, PRO813
CC and PRO11066 induce proliferation of mammalian kidney mesangial cells,
CC and therefore are useful for treating kidney disorders associated with
CC decreased mesangial cell function such as Berger disease or other
CC nephropathies associated with dermatitis, herpetiformis or Crohn's
CC disease. PRO1310, PRO844, PRO1312, PRO1192 and PRO1387 induce the
CC proliferation and/or redifferentiation of chondrocytes in culture and are
CC thus useful for treating sports injuries, and arthritis. This is the
CC amino acid sequence of a novel human PRO protein
XX
SQ Sequence 586 AA;

Query Match 92.5%; Score 2815; DB 6; Length 586;
Best Local Similarity 100.0%; Pred. No. 1.2e-222;
Matches 549; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 MALEIHMSDPMCLIENFNEQLKVNQEALEILSAITQPVVVVAIVGLYRTGKSYLMNKLAG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MALEIHMSDPMCLIENFNEQLKVNQEALEILSAITQPVVVVAIVGLYRTGKSYLMNKLAG 60

Qy         61 KNKGFSVASTVQSHTKGIWIWCVPHPNWPNHTLVLLDTEGLGDVEKADNKNDIQIFALAL 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 KNKGFSVASTVQSHTKGIWIWCVPHPNWPNHTLVLLDTEGLGDVEKADNKNDIQIFALAL 120

Qy        121 LLSSTFVYNTVNKIDQGAIDLLHNVTELTDLLKARNSPDLDRVEDPADSASFFPDLVWTL 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 LLSSTFVYNTVNKIDQGAIDLLHNVTELTDLLKARNSPDLDRVEDPADSASFFPDLVWTL 180

Qy        181 RDFCLGLEIDGQLVTPDEYLENSLRPKQGSDQRVQNFNLPRLCIQKFFPKKKCFIFDLPA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 RDFCLGLEIDGQLVTPDEYLENSLRPKQGSDQRVQNFNLPRLCIQKFFPKKKCFIFDLPA 240

Qy        241 HQKKLAQLETLPDDELEPEFVQQVTEFCSYIFSHSMTKTLPGGIMVNGSRLKNLVLTYVN 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 HQKKLAQLETLPDDELEPEFVQQVTEFCSYIFSHSMTKTLPGGIMVNGSRLKNLVLTYVN 300

Qy        301 AISSGDLPCIENAVLALAQRENSAAVQKAIAHYDQQMGQKVQLPMETLQELLDLHRTSER 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 AISSGDLPCIENAVLALAQRENSAAVQKAIAHYDQQMGQKVQLPMETLQELLDLHRTSER 360

Qy        361 EAIEVFMKNSFKDVDQSFQKELETLLDAKQNDICKRNLEASSDYCSALLKDIFGPLEEAV 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 EAIEVFMKNSFKDVDQSFQKELETLLDAKQNDICKRNLEASSDYCSALLKDIFGPLEEAV 420

Qy        421 KQGIYSKPGGHNLFIQKTEELKAKYYREPRKGIQAEEVLQKYLKSKESVSHAILQTDQAL 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 KQGIYSKPGGHNLFIQKTEELKAKYYREPRKGIQAEEVLQKYLKSKESVSHAILQTDQAL 480

Qy        481 TETEKKKKEAQVKAEAEKAEAQRLAAIQRQNEQMMQERERLHQEQVRQMEIAKQNWLAEQ 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 TETEKKKKEAQVKAEAEKAEAQRLAAIQRQNEQMMQERERLHQEQVRQMEIAKQNWLAEQ 540

Qy        541 QKMQEQQMQ 549
              |||||||||
Db        541 QKMQEQQMQ 549
```

```
RESULT 8
ABO24863
ID   ABO24863 standard; protein; 586 AA.
XX
AC   ABO24863;
XX
DT   05-SEP-2003  (first entry)
XX
DE   Human secreted/transmembrane protein (PRO) #23.
XX
KW   Human; PRO; secreted protein; transmembrane protein; tumour; cytostatic;
KW   gene therapy; tumour necrosis factor-alpha; TNF-alpha; blood;
KW   proteoglycan; cartilage; cytokine; peripheral blood mononuclear cell;
KW   PBMC; glucose uptake; FFA; skeletal muscle cell; adipocyte cell;
KW   chondrocyte cell proliferation; chondrocyte cell differentiation;
KW   pericyte cell; inner ear utricular supporting cell; T-lymphocyte cell;
KW   endothelial cell; A-peptide; factor VIIA.
XX
OS   Homo sapiens.
XX
PN   US2003036179-A1.
XX
PD   20-FEB-2003.
XX
PF   10-MAY-2002; 2002US-00142431.
XX
PR   31-MAR-1997;   97WO-US005230.
PR   12-JUN-1998;   98WO-US012456.
PR   14-JUL-1998;   98WO-US014552.
PR   28-AUG-1998;   98WO-US017888.
PR   10-SEP-1998;   98WO-US018824.
PR   14-SEP-1998;   98WO-US019093.
PR   14-SEP-1998;   98WO-US019094.
PR   14-SEP-1998;   98WO-US019177.
PR   16-SEP-1998;   98WO-US019330.
PR   17-SEP-1998;   98WO-US019437.
PR   07-OCT-1998;   98WO-US021141.
PR   29-OCT-1998;   98WO-US022991.
PR   29-OCT-1998;   98WO-US022992.
PR   20-NOV-1998;   98WO-US024855.
PR   01-DEC-1998;   98WO-US025108.
PR   05-JAN-1999;   99WO-US000106.
PR   08-MAR-1999;   99WO-US005028.
PR   10-MAR-1999;   99WO-US005190.
PR   20-APR-1999;   99WO-US008615.
PR   14-MAY-1999;   99WO-US010733.
PR   02-JUN-1999;   99WO-US012252.
PR   01-SEP-1999;   99WO-US020111.
PR   08-SEP-1999;   99WO-US020594.
PR   13-SEP-1999;   99WO-US020944.
PR   15-SEP-1999;   99WO-US021090.
PR   15-SEP-1999;   99WO-US021547.
PR   05-OCT-1999;   99WO-US023089.
PR   29-NOV-1999;   99WO-US028214.
PR   30-NOV-1999;   99WO-US028313.
PR   30-NOV-1999;   99WO-US028409.
PR   01-DEC-1999;   99WO-US028301.
PR   01-DEC-1999;   99WO-US028634.
PR   02-DEC-1999;   99WO-US028551.
PR   02-DEC-1999;   99WO-US028564.
PR   02-DEC-1999;   99WO-US028565.
PR   16-DEC-1999;   99WO-US030095.
PR   20-DEC-1999;   99WO-US030911.
PR   20-DEC-1999;   99WO-US030999.
PR   22-DEC-1999;   99WO-US030720.
PR   30-DEC-1999;   99WO-US031243.
PR   30-DEC-1999;   99WO-US031274.
PR   05-JAN-2000; 2000WO-US000219.
PR   06-JAN-2000; 2000WO-US000277.
PR   06-JAN-2000; 2000WO-US000376.
PR   11-FEB-2000; 2000WO-US003565.
PR   18-FEB-2000; 2000WO-US004341.
PR   18-FEB-2000; 2000WO-US004342.
PR   22-FEB-2000; 2000WO-US004414.
PR   24-FEB-2000; 2000WO-US004914.
PR   24-FEB-2000; 2000WO-US005004.
PR   01-MAR-2000; 2000WO-US005601.
PR   02-MAR-2000; 2000WO-US005746.
PR   02-MAR-2000; 2000WO-US005841.
PR   10-MAR-2000; 2000WO-US006319.
PR   15-MAR-2000; 2000WO-US006884.
PR   20-MAR-2000; 2000WO-US007377.
PR   21-MAR-2000; 2000WO-US007532.
PR   30-MAR-2000; 2000WO-US008439.
PR   17-MAY-2000; 2000WO-US013705.
PR   22-MAY-2000; 2000WO-US014042.
PR   30-MAY-2000; 2000WO-US014941.
PR   02-JUN-2000; 2000WO-US015264.
PR   28-JUL-2000; 2000WO-US020710.
PR   11-AUG-2000; 2000WO-US022031.
PR   23-AUG-2000; 2000WO-US023522.
PR   24-AUG-2000; 2000WO-US023328.
PR   08-NOV-2000; 2000WO-US030952.
PR   10-NOV-2000; 2000WO-US030873.
PR   01-DEC-2000; 2000WO-US032678.
PR   20-DEC-2000; 2000US-00747259.
PR   20-DEC-2000; 2000WO-US034956.
PR   28-FEB-2001; 2001US-00796498.
PR   28-FEB-2001; 2001WO-US006520.
PR   01-MAR-2001; 2001WO-US006666.
PR   09-MAR-2001; 2001US-00802706.
PR   14-MAR-2001; 2001US-00808689.
PR   22-MAR-2001; 2001US-00816744.
PR   05-APR-2001; 2001US-00828366.
PR   10-MAY-2001; 2001US-00854208.
PR   10-MAY-2001; 2001US-00854280.
PR   18-MAY-2001; 2001US-00860216.
PR   25-MAY-2001; 2001US-00866028.
PR   25-MAY-2001; 2001US-00866034.
PR   25-MAY-2001; 2001WO-US017092.
PR   01-JUN-2001; 2001US-00872035.
PR   01-JUN-2001; 2001WO-US017800.
PR   05-JUN-2001; 2001US-00874503.
PR   14-JUN-2001; 2001US-00882636.
PR   19-JUN-2001; 2001US-00886342.
PR   20-JUN-2001; 2001WO-US019692.
PR   21-JUN-2001; 2001US-00887879.
PR   22-JUN-2001; 2001WO-US020116.
PR   29-JUN-2001; 2001WO-US021066.
PR   09-JUL-2001; 2001WO-US021735.
PR   18-JUL-2001; 2001US-00908827.
PR   06-AUG-2001; 2001US-00924419.
PR   09-AUG-2001; 2001US-00927796.
PR   16-AUG-2001; 2001US-00931836.
PR   19-DEC-2001; 2001US-00028072.
XX
PA   (GETH ) GENENTECH INC.
XX
PI   Baker KP,  Beresini M,  Deforge L,  Desnoyers L,  Filvaroff E,  Gao W;
PI   Gerritsen ME,  Goddard A,  Godowski PJ,  Gurney AL,  Sherwood S;
PI   Smith V,  Stewart TA,  Tumas D,  Watanabe CK,  Wood WI,  Zhang Z;
XX
DR   WPI; 2003-466355/44.
DR   N-PSDB; ACD41817.
XX
PT   New isolated nucleic acid encoding a PRO polypeptide, e.g. PRO1114 or
PT   PRO4978, useful in molecular biology, chromosome and gene mapping, in
PT   generating antisense RNA and DNA, and in gene therapy.
XX
PS   Claim 12; Fig 46; 659pp; English.
XX
CC   The invention relates to an isolated nucleic acid comprising at least 80%
CC   sequence identity to a PRO (secreted and transmembrane protein) cDNA
CC   comprising a nucleic acid (a) encoding a PRO polypeptide, or its
CC   extracellular domain (with or without its associated signal peptide),
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CC   which comprises any of the 275 120-850 residue amino acid sequences,
CC   given in the specification; (b) comprising any of the 275 300-3500
CC   nucleotide sequences, given in the specification; or (c) comprising the
CC   full-length coding sequence of the nucleotide sequences given in the
CC   specification, or of the DNA deposited under any of the American Type
CC   Culture Collection (ATCC) Accession Numbers listed in the specification.
CC   Also included are a vector comprising the novel nucleic acid, a host cell
CC   comprising the vector, producing a PRO polypeptide, the isolated PRO
CC   polypeptides detailed above, a chimaeric molecule comprising the PRO
CC   polypeptide of fused to a heterologous amino acid sequence, an anti-PRO
CC   antibody, detecting a PRO polypeptide in a sample suspected of containing
CC   the PRO polypeptide, linking a bioactive molecule to a cell expressing a
CC   PRO polypeptide, modulating at least one biological activity of a cell
CC   expressing a PRO polypeptide, stimulating the release of tumour necrosis
CC   factor-alpha (TNF-alpha) from human blood, (or proteoglycans from
CC   cartilage or cytokine from peripheral blood mononuclear cells (PBMC)),
CC   modulating the uptake of glucose or FFA by skeletal muscle cells or
CC   adipocyte cells, stimulating the proliferation or differentiation of
CC   chondrocyte cells (or proliferation of or gene expression in pericyte
CC   cells), stimulating the proliferation of inner ear utricular supporting
CC   cells (or of T-lymphocyte cells, or of endothelial cells), inhibiting the
CC   binding of A-peptide to factor VIIA, or differentiation of adipocyte
CC   cells, detecting the presence of a tumour in a mammal and an
CC   oligonucleotide probe derived from any of the nucleotide sequences given
CC   in the specification. The polynucleotide is useful in molecular biology,
CC   including uses as hybridisation probes, in chromosome and gene mapping,
CC   in generating antisense RNA and DNA, and in gene therapy. The
CC   polynucleotide may also be used in preparing PRO polypeptides by
CC   recombinant techniques, and in generating either transgenic animals or
CC   knock-out animals which, in turn, are useful in the development and
CC   screening of therapeutically useful reagents. The PRO polypeptide or the
CC   antibody is used in preparing a medicament for treating a condition
CC   responsive to the polypeptide or antibody, such as tumours, and in
CC   various diagnostic assays. The present sequence rperesents a PRO
CC   polypeptide
XX
SQ   Sequence 586 AA;

  Query Match             92.5%;  Score 2815;  DB 6;  Length 586;
  Best Local Similarity   100.0%;  Pred. No. 1.2e-222;
  Matches  549;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MALEIHMSDPMCLIENFNEQLKVNQEALEILSAITQPVVVVAIVGLYRTGKSYLMNKLAG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MALEIHMSDPMCLIENFNEQLKVNQEALEILSAITQPVVVVAIVGLYRTGKSYLMNKLAG 60

Qy         61 KNKGFSVASTVQSHTKGIWIWCVPHPNWPNHTLVLLDTEGLGDVEKADNKNDIQIFALAL 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 KNKGFSVASTVQSHTKGIWIWCVPHPNWPNHTLVLLDTEGLGDVEKADNKNDIQIFALAL 120

Qy        121 LLSSTFVYNTVNKIDQGAIDLLHNVTELTDLLKARNSPDLDRVEDPADSASFFPDLVWTL 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 LLSSTFVYNTVNKIDQGAIDLLHNVTELTDLLKARNSPDLDRVEDPADSASFFPDLVWTL 180

Qy        181 RDFCLGLEIDGQLVTPDEYLENSLRPKQGSDQRVQNFNLPRLCIQKFFPKKKCFIFDLPA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 RDFCLGLEIDGQLVTPDEYLENSLRPKQGSDQRVQNFNLPRLCIQKFFPKKKCFIFDLPA 240

Qy        241 HQKKLAQLETLPDDELEPEFVQQVTEFCSYIFSHSMTKTLPGGIMVNGSRLKNLVLTYVN 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 HQKKLAQLETLPDDELEPEFVQQVTEFCSYIFSHSMTKTLPGGIMVNGSRLKNLVLTYVN 300

Qy        301 AISSGDLPCIENAVLALAQRENSAAVQKAIAHYDQQMGQKVQLPMETLQELLDLHRTSER 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 AISSGDLPCIENAVLALAQRENSAAVQKAIAHYDQQMGQKVQLPMETLQELLDLHRTSER 360

Qy        361 EAIEVFMKNSFKDVDQSFQKELETLLDAKQNDICKRNLEASSDYCSALLKDIFGPLEEAV 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 EAIEVFMKNSFKDVDQSFQKELETLLDAKQNDICKRNLEASSDYCSALLKDIFGPLEEAV 420

Qy        421 KQGIYSKPGGHNLFIQKTEELKAKYYREPRKGIQAEEVLQKYLKSKESVSHAILQTDQAL 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 KQGIYSKPGGHNLFIQKTEELKAKYYREPRKGIQAEEVLQKYLKSKESVSHAILQTDQAL 480

Qy        481 TETEKKKKEAQVKAEAEKAEAQRLAAIQRQNEQMMQERERLHQEQVRQMEIAKQNWLAEQ 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 TETEKKKKEAQVKAEAEKAEAQRLAAIQRQNEQMMQERERLHQEQVRQMEIAKQNWLAEQ 540

Qy        541 QKMQEQQMQ 549
              |||||||||
Db        541 QKMQEQQMQ 549


RESULT 9
ABU66868
ID   ABU66868 standard; protein; 586 AA.
XX
AC   ABU66868;
XX
DT   27-MAY-2003  (first entry)
XX
DE   Human secreted/transmembrane, PRO, protein SEQ ID 46.
XX
KW   Human; secreted protein; transmembrane protein; PRO;
KW   inflammatory disease; organ failure; atherosclerosis; cardiac injury;
KW   infertility; birth defects; premature aging; AIDS; biosensor;
KW   acquired immunodeficiency syndrome; cancer; diabetic complication;
KW   bioreactor; tumour.
XX
OS   Homo sapiens.
XX
PN   US2003032155-A1.
XX
PD   13-FEB-2003.
XX
PF   03-MAY-2002; 2002US-00137865.
XX
PR   31-MAR-1997;   97WO-US005230.
PR   12-JUN-1998;   98WO-US012456.
PR   14-JUL-1998;   98WO-US014552.
PR   28-AUG-1998;   98WO-US017888.
PR   10-SEP-1998;   98WO-US018824.
PR   14-SEP-1998;   98WO-US019093.
PR   14-SEP-1998;   98WO-US019094.
PR   14-SEP-1998;   98WO-US019177.
PR   16-SEP-1998;   98WO-US019330.
PR   17-SEP-1998;   98WO-US019437.
PR   07-OCT-1998;   98WO-US021141.
PR   29-OCT-1998;   98WO-US022991.
PR   29-OCT-1998;   98WO-US022992.
PR   20-NOV-1998;   98WO-US024855.
PR   01-DEC-1998;   98WO-US025108.
PR   05-JAN-1999;   99WO-US000106.
PR   08-MAR-1999;   99WO-US005028.
PR   10-MAR-1999;   99WO-US005190.
PR   20-APR-1999;   99WO-US008615.
PR   14-MAY-1999;   99WO-US010733.
PR   02-JUN-1999;   99WO-US012252.
PR   01-SEP-1999;   99WO-US020111.
PR   08-SEP-1999;   99WO-US020594.
PR   13-SEP-1999;   99WO-US020944.
PR   15-SEP-1999;   99WO-US021090.
PR   15-SEP-1999;   99WO-US021547.
PR   05-OCT-1999;   99WO-US023089.
PR   29-NOV-1999;   99WO-US028214.
PR   30-NOV-1999;   99WO-US028313.
PR   30-NOV-1999;   99WO-US028409.
PR   01-DEC-1999;   99WO-US028301.
PR   01-DEC-1999;   99WO-US028634.
PR   02-DEC-1999;   99WO-US028551.
PR   02-DEC-1999;   99WO-US028564.
PR   02-DEC-1999;   99WO-US028565.
PR   16-DEC-1999;   99WO-US030095.
PR   20-DEC-1999;   99WO-US030911.
PR   20-DEC-1999;   99WO-US030999.
PR   22-DEC-1999;   99WO-US030720.
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PR 30-DEC-1999; 99WO-US031243.
PR 30-DEC-1999; 99WO-US031274.
PR 05-JAN-2000; 2000WO-US000219.
PR 06-JAN-2000; 2000WO-US000277.
PR 06-JAN-2000; 2000WO-US000376.
PR 11-FEB-2000; 2000WO-US003565.
PR 18-FEB-2000; 2000WO-US004341.
PR 18-FEB-2000; 2000WO-US004342.
PR 22-FEB-2000; 2000WO-US004414.
PR 24-FEB-2000; 2000WO-US004914.
PR 24-FEB-2000; 2000WO-US005004.
PR 01-MAR-2000; 2000WO-US005601.
PR 02-MAR-2000; 2000WO-US005746.
PR 02-MAR-2000; 2000WO-US005841.
PR 10-MAR-2000; 2000WO-US006319.
PR 15-MAR-2000; 2000WO-US006884.
PR 20-MAR-2000; 2000WO-US007377.
PR 21-MAR-2000; 2000WO-US007532.
PR 30-MAR-2000; 2000WO-US008439.
PR 17-MAY-2000; 2000WO-US013705.
PR 22-MAY-2000; 2000WO-US014042.
PR 30-MAY-2000; 2000WO-US014941.
PR 02-JUN-2000; 2000WO-US015264.
PR 28-JUL-2000; 2000WO-US020710.
PR 11-AUG-2000; 2000WO-US022031.
PR 23-AUG-2000; 2000WO-US023522.
PR 24-AUG-2000; 2000WO-US023328.
PR 08-NOV-2000; 2000WO-US030952.
PR 10-NOV-2000; 2000WO-US030873.
PR 01-DEC-2000; 2000WO-US032678.
PR 20-DEC-2000; 2000US-00747259.
PR 20-DEC-2000; 2000WO-US034956.
PR 28-FEB-2001; 2001US-00796498.
PR 28-FEB-2001; 2001WO-US006520.
PR 01-MAR-2001; 2001WO-US006666.
PR 09-MAR-2001; 2001US-00802706.
PR 14-MAR-2001; 2001US-00808689.
PR 22-MAR-2001; 2001US-00816744.
PR 05-APR-2001; 2001US-00828366.
PR 10-MAY-2001; 2001US-00854208.
PR 10-MAY-2001; 2001US-00854280.
PR 18-MAY-2001; 2001US-00860216.
PR 25-MAY-2001; 2001US-00866028.
PR 25-MAY-2001; 2001US-00866034.
PR 25-MAY-2001; 2001WO-US017092.
PR 01-JUN-2001; 2001US-00872035.
PR 01-JUN-2001; 2001WO-US017800.
PR 05-JUN-2001; 2001US-00874503.
PR 14-JUN-2001; 2001US-00882636.
PR 19-JUN-2001; 2001US-00886342.
PR 20-JUN-2001; 2001WO-US019692.
PR 21-JUN-2001; 2001US-00887879.
PR 22-JUN-2001; 2001WO-US020116.
PR 29-JUN-2001; 2001WO-US021066.
PR 09-JUL-2001; 2001WO-US021735.
PR 18-JUL-2001; 2001US-00908827.
PR 06-AUG-2001; 2001US-00924419.
PR 09-AUG-2001; 2001US-00927796.
PR 16-AUG-2001; 2001US-00931836.
PR 19-DEC-2001; 2001US-00028072.
XX
PA (GETH) GENENTECH INC.
XX
PI Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, Gao W;
PI Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;
PI Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;
XX
DR WPI; 2003-331925/31.
DR N-PSDB; ACA04046.
XX
PT New secreted and transmembrane nucleic acids and polypeptides, designated
PT as PRO, useful for treating inflammation, organ failure, atherosclerosis,
PT cardiac injury, infertility, birth defects, premature aging, AIDS, or
PT cancer.
XX
PS Claim 12; Fig 46; 659pp; English.
XX
CC The invention relates to an isolated nucleic acid comprising, or which is
CC at least 80% identical to, or the full-length coding sequence of, any of
CC the 275 nucleotide sequences, encoding the corresponding PRO polypeptide
CC (one of 275 secreted or transmembrane proteins). The nucleic acid further
CC comprises the full-length coding sequence of the DNA deposited under
CC American Type Culture Collection (ATCC) accession number in a list given
CC in the specification. Also included are vectors and host cells for
CC producing PRO proteins, PRO fusion proteins, anti-PRO antibodies, PRO
CC extracellular domains and mature sequences, methods of detecting PRO
CC proteins, methods for stimulating the release of TNF-alpha (tumour
CC necrosis factor alpha) from human blood, (and the proliferation of
CC differentiation of chondrocyte cells, the proliferation of, or gene
CC expression in pericyte cells, the release or proteoglycans from
CC cartilage, proliferation of inner ear urticular supporting cells, the
CC proliferation of T-lymphocyte cells, the release of a cytokine from
CC peripheral blood mononuclear cells (PBMC), or the proliferation of
CC endothelial cells), a method for modulating the uptake of glucose or free
CC fatty acid (FFA) by skeletal muscle cells, a method for inhibiting the
CC binding of A-peptide to factor VIIA, or the differentiation of adipocyte
CC cells, a method for detecting the presence of a tumour in a mammal and an
CC oligonucleotide probe derived from any of the nucleotide sequences cited
CC above. The nucleic acids and polypeptides are useful for treating
CC inflammatory diseases, organ failure, atherosclerosis, cardiac injury,
CC infertility, birth defects, premature aging, AIDS (acquired
CC immunodeficiency syndrome), cancer, or diabetic complications. The
CC nucleic acids are useful as hybridisation probes, in chromosome and gene
CC mapping, and in generating antisense RNA or DNA. The polypeptides are
CC useful as pharmaceuticals, diagnostics, biosensors or bioreactors. Both
CC are useful in tissue typing. The present sequence represents a PRO
CC protein of the invention
XX
SQ Sequence 586 AA;

Query Match 92.5%; Score 2815; DB 6; Length 586;
Best Local Similarity 100.0%; Pred. No. 1.2e-222;
Matches 549; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 MALEIHMSDPMCLIENFNEQLKVNQEALEILSAITQPVVVVAIVGLYRTGKSYLMNKLAG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MALEIHMSDPMCLIENFNEQLKVNQEALEILSAITQPVVVVAIVGLYRTGKSYLMNKLAG 60

Qy         61 KNKGFSVASTVQSHTKGIWIWCVPHPNWPNHTLVLLDTEGLGDVEKADNKNDIQIFALAL 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 KNKGFSVASTVQSHTKGIWIWCVPHPNWPNHTLVLLDTEGLGDVEKADNKNDIQIFALAL 120

Qy        121 LLSSTFVYNTVNKIDQGAIDLLHNVTELTDLLKARNSPDLDRVEDPADSASFFPDLVWTL 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 LLSSTFVYNTVNKIDQGAIDLLHNVTELTDLLKARNSPDLDRVEDPADSASFFPDLVWTL 180

Qy        181 RDFCLGLEIDGQLVTPDEYLENSLRPKQGSDQRVQNFNLPRLCIQKFFPKKKCFIFDLPA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 RDFCLGLEIDGQLVTPDEYLENSLRPKQGSDQRVQNFNLPRLCIQKFFPKKKCFIFDLPA 240

Qy        241 HQKKLAQLETLPDDELEPEFVQQVTEFCSYIFSHSMTKTLPGGIMVNGSRLKNLVLTYVN 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 HQKKLAQLETLPDDELEPEFVQQVTEFCSYIFSHSMTKTLPGGIMVNGSRLKNLVLTYVN 300

Qy        301 AISSGDLPCIENAVLALAQRENSAAVQKAIAHYDQQMGQKVQLPMETLQELLDLHRTSER 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 AISSGDLPCIENAVLALAQRENSAAVQKAIAHYDQQMGQKVQLPMETLQELLDLHRTSER 360

Qy        361 EAIEVFMKNSFKDVDQSFQKELETLLDAKQNDICKRNLEASSDYCSALLKDIFGPLEEAV 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 EAIEVFMKNSFKDVDQSFQKELETLLDAKQNDICKRNLEASSDYCSALLKDIFGPLEEAV 420

Qy        421 KQGIYSKPGGHNLFIQKTEELKAKYYREPRKGIQAEEVLQKYLKSKESVSHAILQTDQAL 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 KQGIYSKPGGHNLFIQKTEELKAKYYREPRKGIQAEEVLQKYLKSKESVSHAILQTDQAL 480
```

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Qy        481 TETEKKKKEAQVKAEAEKAEAQRLAAIQRQNEQMMQERERLHQEQVRQMEIAKQNWLAEQ 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 TETEKKKKEAQVKAEAEKAEAQRLAAIQRQNEQMMQERERLHQEQVRQMEIAKQNWLAEQ 540

Qy        541 QKMQEQQMQ 549
              |||||||||
Db        541 QKMQEQQMQ 549


RESULT 10
ADA45565
ID   ADA45565 standard; protein; 586 AA.
XX
AC   ADA45565;
XX
DT   20-NOV-2003  (first entry)
XX
DE   Novel human secreted and transmembrane protein PRO4987.
XX
KW   Human; secreted and transmembrane protein; PRO;
KW   Tumour necrosis factor alpha release; TNF-alpha release;
KW   glucose uptake modulator; FFA uptake modulator;
KW   cell proliferation stimulator; cell differentiation stimulator;
KW   cell differentiation inihibitor; cytokine release stimulator; tumour;
KW   lung tumoue; colon tumour; breast tumour; prostate tumour; rectal tumour;
KW   cervical tumour; liver tumour; chromosome mapping; gene mapping;
KW   gene therapy; chromosome identification; chromosome marker.
XX
OS   Homo sapiens.
XX
PN   US2003022328-A1.
XX
PD   30-JAN-2003.
XX
PF   16-APR-2002; 2002US-00123904.
XX
PR   31-MAR-1997;   97WO-US005230.
PR   12-JUN-1998;   98WO-US012456.
PR   14-JUL-1998;   98WO-US014552.
PR   28-AUG-1998;   98WO-US017888.
PR   10-SEP-1998;   98WO-US018824.
PR   14-SEP-1998;   98WO-US019093.
PR   14-SEP-1998;   98WO-US019094.
PR   14-SEP-1998;   98WO-US019177.
PR   16-SEP-1998;   98WO-US019330.
PR   17-SEP-1998;   98WO-US019437.
PR   07-OCT-1998;   98WO-US021141.
PR   29-OCT-1998;   98WO-US022991.
PR   29-OCT-1998;   98WO-US022992.
PR   20-NOV-1998;   98WO-US024855.
PR   01-DEC-1998;   98WO-US025108.
PR   05-JAN-1999;   99WO-US000106.
PR   08-MAR-1999;   99WO-US005028.
PR   10-MAR-1999;   99WO-US005190.
PR   20-APR-1999;   99WO-US008615.
PR   14-MAY-1999;   99WO-US010733.
PR   02-JUN-1999;   99WO-US012252.
PR   01-SEP-1999;   99WO-US020111.
PR   08-SEP-1999;   99WO-US020594.
PR   13-SEP-1999;   99WO-US020944.
PR   15-SEP-1999;   99WO-US021090.
PR   15-SEP-1999;   99WO-US021547.
PR   05-OCT-1999;   99WO-US023089.
PR   29-NOV-1999;   99WO-US028214.
PR   30-NOV-1999;   99WO-US028313.
PR   30-NOV-1999;   99WO-US028409.
PR   01-DEC-1999;   99WO-US028301.
PR   01-DEC-1999;   99WO-US028634.
PR   02-DEC-1999;   99WO-US028551.
PR   02-DEC-1999;   99WO-US028564.
PR   02-DEC-1999;   99WO-US028565.
PR   16-DEC-1999;   99WO-US030095.
PR   20-DEC-1999;   99WO-US030911.
PR   20-DEC-1999;   99WO-US030999.
PR   22-DEC-1999;   99WO-US030720.
PR   30-DEC-1999;   99WO-US031243.
PR   30-DEC-1999;   99WO-US031274.
PR   05-JAN-2000; 2000WO-US000219.
PR   06-JAN-2000; 2000WO-US000277.
PR   06-JAN-2000; 2000WO-US000376.
PR   11-FEB-2000; 2000WO-US003565.
PR   18-FEB-2000; 2000WO-US004341.
PR   18-FEB-2000; 2000WO-US004342.
PR   22-FEB-2000; 2000WO-US004414.
PR   24-FEB-2000; 2000WO-US004914.
PR   24-FEB-2000; 2000WO-US005004.
PR   01-MAR-2000; 2000WO-US005601.
PR   02-MAR-2000; 2000WO-US005746.
PR   02-MAR-2000; 2000WO-US005841.
PR   10-MAR-2000; 2000WO-US006319.
PR   15-MAR-2000; 2000WO-US006884.
PR   20-MAR-2000; 2000WO-US007377.
PR   21-MAR-2000; 2000WO-US007532.
PR   30-MAR-2000; 2000WO-US008439.
PR   17-MAY-2000; 2000WO-US013705.
PR   22-MAY-2000; 2000WO-US014042.
PR   30-MAY-2000; 2000WO-US014941.
PR   02-JUN-2000; 2000WO-US015264.
PR   28-JUL-2000; 2000WO-US020710.
PR   11-AUG-2000; 2000WO-US022031.
PR   23-AUG-2000; 2000WO-US023522.
PR   24-AUG-2000; 2000WO-US023328.
PR   08-NOV-2000; 2000WO-US030952.
PR   10-NOV-2000; 2000WO-US030873.
PR   01-DEC-2000; 2000WO-US032678.
PR   20-DEC-2000; 2000US-00747259.
PR   20-DEC-2000; 2000WO-US034956.
PR   28-FEB-2001; 2001US-00796498.
PR   28-FEB-2001; 2001WO-US006520.
PR   01-MAR-2001; 2001WO-US006666.
PR   09-MAR-2001; 2001US-00802706.
PR   14-MAR-2001; 2001US-00808689.
PR   22-MAR-2001; 2001US-00816744.
PR   05-APR-2001; 2001US-00828366.
PR   10-MAY-2001; 2001US-00854208.
PR   10-MAY-2001; 2001US-00854280.
PR   18-MAY-2001; 2001US-00860216.
PR   25-MAY-2001; 2001US-00866028.
PR   25-MAY-2001; 2001US-00866034.
PR   25-MAY-2001; 2001WO-US017092.
PR   01-JUN-2001; 2001US-00872035.
PR   01-JUN-2001; 2001WO-US017800.
PR   05-JUN-2001; 2001US-00874503.
PR   14-JUN-2001; 2001US-00882636.
PR   19-JUN-2001; 2001US-00886342.
PR   20-JUN-2001; 2001WO-US019692.
PR   21-JUN-2001; 2001US-00887879.
PR   22-JUN-2001; 2001WO-US020116.
PR   29-JUN-2001; 2001WO-US021066.
PR   09-JUL-2001; 2001WO-US021735.
PR   18-JUL-2001; 2001US-00908827.
PR   06-AUG-2001; 2001US-00924419.
PR   09-AUG-2001; 2001US-00927796.
PR   16-AUG-2001; 2001US-00931836.
PR   19-DEC-2001; 2001US-00028072.
XX
PA   (GETH ) GENENTECH INC.
XX
PI   Baker KP,  Beresini M,  Deforge L,  Desnoyers L,  Filvaroff E,  Gao W;
PI   Gerritsen ME,  Goddard A,  Godowski PJ,  Gurney AL,  Sherwood S;
PI   Smith V,  Stewart TA,  Tumas D,  Watanabe CK,  Wood WI,  Zhang Z;
XX
DR   WPI; 2003-584997/55.
DR   N-PSDB; ADA45564.
XX
PT   Novel secreted and transmembrane polypeptide for modulating biological
```

```
PT   activity of cell expressing the polypeptide, identifying agonists or
PT   antagonists of polypeptide, and as molecular weight markers.
XX
PS   Claim 12; Fig 46; 659pp; English.
XX
CC   The invention describes 305 nucleic acids encoding PRO (secreted and
CC   transmembrane) polypeptides (I). (I) is useful for stimulating the
CC   release of TNF-alpha from human blood, for modulating the uptake of
CC   glucose or FFA by skeletal muscle cells or adipocyte cells, for
CC   stimulating the proliferation or differentiation of chondrocyte cells,
CC   for stimulating the proliferation of or gene expression in pericyte
CC   cells, for stimulating the release of proteoglycans from cartilage, for
CC   stimulating the proliferation of inner ear utricular supporting cells,
CC   for stimulating the proliferation of T-lymphocyte cells, for stimulating
CC   the release of a cytokine from PBMC cells, for inhibiting the binding of
CC   A-peptide to factor VIIA, for inhibiting the differentiation of adipocyte
CC   cells, for stimulating proliferation of endothelial cells, for detecting
CC   the presence of tumour in a mammal. The tumour is lung, colon, breast,
CC   prostate, rectal, cervical or liver tumour. The oligonucleotide probes
CC   are useful for isolating genomic and cDNA nucleotide sequences or
CC   antisense probes. (I) is also useful as therapeutic agent. PRO is useful
CC   in assays to identify other proteins or molecules involved in binding
CC   interaction. A polynucleotide (II) encoding (I) is useful in chromosome
CC   and gene mapping, in generation of antisense RNA and DNA, in the
CC   preparation of PRO polypeptide, for generating transgenic animals or
CC   knockout animals which in turn are useful in the development and
CC   screening of therapeutically useful reagents, in gene therapy, for
CC   chromosome identification, as chromosome marker, and for generating
CC   probes. An anti-(I)-antibody is useful in diagnostic assays for PRO, e.g.
CC   detecting its expression in specific cells, tissues or serum, and for
CC   affinity purification of PRO from recombinant cell culture or natural
CC   sources. (I) and (II) are useful for tissue typing. This is the amino
CC   acid sequence of a novel human secreted and transmembrane PRO
CC   polypeptide.
XX
SQ   Sequence 586 AA;

  Query Match             92.5%;  Score 2815;  DB 6;  Length 586;
  Best Local Similarity   100.0%;  Pred. No. 1.2e-222;
  Matches  549;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MALEIHMSDPMCLIENFNEQLKVNQEALEILSAITQPVVVVAIVGLYRTGKSYLMNKLAG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MALEIHMSDPMCLIENFNEQLKVNQEALEILSAITQPVVVVAIVGLYRTGKSYLMNKLAG 60

Qy         61 KNKGFSVASTVQSHTKGIWIWCVPHPNWPNHTLVLLDTEGLGDVEKADNKNDIQIFALAL 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 KNKGFSVASTVQSHTKGIWIWCVPHPNWPNHTLVLLDTEGLGDVEKADNKNDIQIFALAL 120

Qy        121 LLSSTFVYNTVNKIDQGAIDLLHNVTELTDLLKARNSPDLDRVEDPADSASFFPDLVWTL 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 LLSSTFVYNTVNKIDQGAIDLLHNVTELTDLLKARNSPDLDRVEDPADSASFFPDLVWTL 180

Qy        181 RDFCLGLEIDGQLVTPDEYLENSLRPKQGSDQRVQNFNLPRLCIQKFFPKKKCFIFDLPA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 RDFCLGLEIDGQLVTPDEYLENSLRPKQGSDQRVQNFNLPRLCIQKFFPKKKCFIFDLPA 240

Qy        241 HQKKLAQLETLPDDELEPEFVQQVTEFCSYIFSHSMTKTLPGGIMVNGSRLKNLVLTYVN 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 HQKKLAQLETLPDDELEPEFVQQVTEFCSYIFSHSMTKTLPGGIMVNGSRLKNLVLTYVN 300

Qy        301 AISSGDLPCIENAVLALAQRENSAAVQKAIAHYDQQMGQKVQLPMETLQELLDLHRTSER 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 AISSGDLPCIENAVLALAQRENSAAVQKAIAHYDQQMGQKVQLPMETLQELLDLHRTSER 360

Qy        361 EAIEVFMKNSFKDVDQSFQKELETLLDAKQNDICKRNLEASSDYCSALLKDIFGPLEEAV 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 EAIEVFMKNSFKDVDQSFQKELETLLDAKQNDICKRNLEASSDYCSALLKDIFGPLEEAV 420

Qy        421 KQGIYSKPGGHNLFIQKTEELKAKYYREPRKGIQAEEVLQKYLKSKESVSHAILQTDQAL 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 KQGIYSKPGGHNLFIQKTEELKAKYYREPRKGIQAEEVLQKYLKSKESVSHAILQTDQAL 480

Qy        481 TETEKKKKEAQVKAEAEKAEAQRLAAIQRQNEQMMQERERLHQEQVRQMEIAKQNWLAEQ 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 TETEKKKKEAQVKAEAEKAEAQRLAAIQRQNEQMMQERERLHQEQVRQMEIAKQNWLAEQ 540

Qy        541 QKMQEQQMQ 549
              |||||||||
Db        541 QKMQEQQMQ 549


RESULT 11
ADA75996
ID   ADA75996 standard; protein; 586 AA.
XX
AC   ADA75996;
XX
DT   20-NOV-2003  (first entry)
XX
DE   Human PRO polypeptide #23.
XX
KW   Human; PRO; secreted polypeptide; transmembrane polypeptide;
KW   tumour necrosis factor-alpha; TNF-alpha; chondrocyte cell; tumour;
KW   cancer; adrenal; lung; colon; breast; prostate; rectum; kidney; cervix;
KW   liver; microvascular endothelial cell; glucose; FFA;
KW   skeletal muscle cell; adipocyte cell; pericyte cell;
KW   inner ear utricular supporting cell; T-lymphocyte cell;
KW   endothelial cell tube formation; bone disorder; cartilage disorder;
KW   sports injury; proteoglycan; articular cartilage defect; osteoarthritis;
KW   rheumatoid arthritis; haemoglobin-associated disorder thalassaemia;
KW   immune system cell infiltration.
XX
OS   Homo sapiens.
XX
PN   US2003073212-A1.
XX
PD   17-APR-2003.
XX
PF   16-APR-2002; 2002US-00123903.
XX
PR   31-MAR-1997;   97WO-US005230.
PR   12-JUN-1998;   98WO-US012456.
PR   14-JUL-1998;   98WO-US014552.
PR   28-AUG-1998;   98WO-US017888.
PR   10-SEP-1998;   98WO-US018824.
PR   14-SEP-1998;   98WO-US019093.
PR   14-SEP-1998;   98WO-US019094.
PR   14-SEP-1998;   98WO-US019177.
PR   16-SEP-1998;   98WO-US019330.
PR   17-SEP-1998;   98WO-US019437.
PR   07-OCT-1998;   98WO-US021141.
PR   29-OCT-1998;   98WO-US022991.
PR   29-OCT-1998;   98WO-US022992.
PR   20-NOV-1998;   98WO-US024855.
PR   01-DEC-1998;   98WO-US025108.
PR   05-JAN-1999;   99WO-US000106.
PR   08-MAR-1999;   99WO-US005028.
PR   10-MAR-1999;   99WO-US005190.
PR   20-APR-1999;   99WO-US008615.
PR   14-MAY-1999;   99WO-US010733.
PR   02-JUN-1999;   99WO-US012252.
PR   01-SEP-1999;   99WO-US020111.
PR   08-SEP-1999;   99WO-US020594.
PR   13-SEP-1999;   99WO-US020944.
PR   15-SEP-1999;   99WO-US021090.
PR   15-SEP-1999;   99WO-US021547.
PR   05-OCT-1999;   99WO-US023089.
PR   29-NOV-1999;   99WO-US028214.
PR   30-NOV-1999;   99WO-US028313.
PR   30-NOV-1999;   99WO-US028409.
PR   01-DEC-1999;   99WO-US028301.
PR   01-DEC-1999;   99WO-US028634.
PR   02-DEC-1999;   99WO-US028551.
PR   02-DEC-1999;   99WO-US028564.
PR   02-DEC-1999;   99WO-US028565.
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PR 16-DEC-1999; 99WO-US030095.
PR 20-DEC-1999; 99WO-US030911.
PR 20-DEC-1999; 99WO-US030999.
PR 22-DEC-1999; 99WO-US030720.
PR 30-DEC-1999; 99WO-US031243.
PR 30-DEC-1999; 99WO-US031274.
PR 05-JAN-2000; 2000WO-US000219.
PR 06-JAN-2000; 2000WO-US000277.
PR 06-JAN-2000; 2000WO-US000376.
PR 11-FEB-2000; 2000WO-US003565.
PR 18-FEB-2000; 2000WO-US004341.
PR 18-FEB-2000; 2000WO-US004342.
PR 22-FEB-2000; 2000WO-US004414.
PR 24-FEB-2000; 2000WO-US004914.
PR 24-FEB-2000; 2000WO-US005004.
PR 01-MAR-2000; 2000WO-US005601.
PR 02-MAR-2000; 2000WO-US005746.
PR 02-MAR-2000; 2000WO-US005841.
PR 10-MAR-2000; 2000WO-US006319.
PR 15-MAR-2000; 2000WO-US006884.
PR 20-MAR-2000; 2000WO-US007377.
PR 21-MAR-2000; 2000WO-US007532.
PR 30-MAR-2000; 2000WO-US008439.
PR 17-MAY-2000; 2000WO-US013705.
PR 22-MAY-2000; 2000WO-US014042.
PR 30-MAY-2000; 2000WO-US014941.
PR 02-JUN-2000; 2000WO-US015264.
PR 28-JUL-2000; 2000WO-US020710.
PR 11-AUG-2000; 2000WO-US022031.
PR 23-AUG-2000; 2000WO-US023522.
PR 24-AUG-2000; 2000WO-US023328.
PR 08-NOV-2000; 2000WO-US030952.
PR 10-NOV-2000; 2000WO-US030873.
PR 01-DEC-2000; 2000WO-US032678.
PR 20-DEC-2000; 2000US-00747259.
PR 20-DEC-2000; 2000WO-US034956.
PR 28-FEB-2001; 2001US-00796498.
PR 28-FEB-2001; 2001WO-US006520.
PR 01-MAR-2001; 2001WO-US006666.
PR 09-MAR-2001; 2001US-00802706.
PR 14-MAR-2001; 2001US-00808689.
PR 22-MAR-2001; 2001US-00816744.
PR 05-APR-2001; 2001US-00828366.
PR 10-MAY-2001; 2001US-00854208.
PR 10-MAY-2001; 2001US-00854280.
PR 18-MAY-2001; 2001US-00860216.
PR 25-MAY-2001; 2001US-00866028.
PR 25-MAY-2001; 2001US-00866034.
PR 25-MAY-2001; 2001WO-US017092.
PR 01-JUN-2001; 2001US-00872035.
PR 01-JUN-2001; 2001WO-US017800.
PR 05-JUN-2001; 2001US-00874503.
PR 14-JUN-2001; 2001US-00882636.
PR 19-JUN-2001; 2001US-00886342.
PR 20-JUN-2001; 2001WO-US019692.
PR 21-JUN-2001; 2001US-00887879.
PR 22-JUN-2001; 2001WO-US020116.
PR 29-JUN-2001; 2001WO-US021066.
PR 09-JUL-2001; 2001WO-US021735.
PR 18-JUL-2001; 2001US-00908827.
PR 06-AUG-2001; 2001US-00924419.
PR 09-AUG-2001; 2001US-00927796.
PR 16-AUG-2001; 2001US-00931836.
PR 19-DEC-2001; 2001US-00028072.
XX
PA (GETH) GENENTECH INC.
XX
PI Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, Gao W;
PI Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;
PI Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;
XX
DR WPI; 2003-687639/65.
DR N-PSDB; ADA75995.

XX
PT New isolated nucleic acid encoding a secreted and transmembrane
PT polypeptide, designated e.g. PRO1114 or PRO4978, useful in chromosome and
PT gene mapping, in generating antisense RNA and DNA, and in gene therapy.
XX
PS Claim 12; Fig 46; 659pp; English.
XX
CC The invention relates to isolated human PRO polypeptides (secreted and
CC transmembrane polypeptides) and the polynucleotides encoding them. The
CC invention also relates to an antibody which specifically binds to a PRO
CC polypeptide, a method for stimulating the release of tumour necrosis
CC factor-alpha (TNF-alpha) from human blood, a method for stimulating the
CC proliferation or differentiation of chondrocyte cells and a method for
CC detecting the presence of a tumour in a mammal (e.g. adrenal, lung,
CC colon, breast, prostate, rectal, kidney, cervical and liver tumours). The
CC polynucleotides are useful in molecular biology, including uses as
CC hybridisation probes, in chromosome and gene mapping, in generating
CC antisense RNA and DNA and in gene therapy. The polynucleotides may also
CC be used in preparing PRO polypeptides by recombinant techniques and in
CC generating either transgenic animals or knock-out animals which are
CC useful in the development and screening of therapeutically useful
CC reagents. The PRO polypeptides or antibodies are used in preparing a
CC medicament for treating a condition responsive to the polypeptides or
CC antibodies, such as tumours, for stimulating and inhibiting proliferation
CC of human microvascular endothelial cells, for modulating the uptake of
CC glucose or FFA by skeletal muscle cells or adipocyte cells, for
CC stimulating differentiation of adipocyte cells, for stimulating
CC proliferation of or gene expression in pericyte cells, for stimulating
CC the proliferation of inner ear utricular supporting cells or T-lymphocyte
CC cells, for inducing endothelial cell tube formation and for treating
CC various bone and/or cartilage disorders such as sports injuries and
CC arthritis. PRO polypeptides which stimulate the release of proteoglycans
CC from cartilage are useful for treating sports-related joint problems,
CC articular cartilage defects, osteoarthritis and rheumatoid arthritis. PRO
CC polypeptides are also useful for treating various mammalian haemoglobin-
CC associated disorders such as various thalassaemias and conditions which
CC may benefit from enhanced local immune system cell infiltration. This
CC sequence represents a human PRO polypeptide of the invention. Note: The
CC sequence data for this patent is also available in electronic format from
CC USPTO at seqdata.uspto.gov/sequence.html.
XX
SQ Sequence 586 AA;

Query Match 92.5%; Score 2815; DB 6; Length 586;
Best Local Similarity 100.0%; Pred. No. 1.2e-222;
Matches 549; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 MALEIHMSDPMCLIENFNEQLKVNQEALEILSAITQPVVVVAIVGLYRTGKSYLMNKLAG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MALEIHMSDPMCLIENFNEQLKVNQEALEILSAITQPVVVVAIVGLYRTGKSYLMNKLAG 60

Qy         61 KNKGFSVASTVQSHTKGIWIWCVPHPNWPNHTLVLLDTEGLGDVEKADNKNDIQIFALAL 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 KNKGFSVASTVQSHTKGIWIWCVPHPNWPNHTLVLLDTEGLGDVEKADNKNDIQIFALAL 120

Qy        121 LLSSTFVYNTVNKIDQGAIDLLHNVTELTDLLKARNSPDLDRVEDPADSASFFPDLVWTL 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 LLSSTFVYNTVNKIDQGAIDLLHNVTELTDLLKARNSPDLDRVEDPADSASFFPDLVWTL 180

Qy        181 RDFCLGLEIDGQLVTPDEYLENSLRPKQGSDQRVQNFNLPRLCIQKFFPKKKCFIFDLPA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 RDFCLGLEIDGQLVTPDEYLENSLRPKQGSDQRVQNFNLPRLCIQKFFPKKKCFIFDLPA 240

Qy        241 HQKKLAQLETLPDDELEPEFVQQVTEFCSYIFSHSMTKTLPGGIMVNGSRLKNLVLTYVN 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 HQKKLAQLETLPDDELEPEFVQQVTEFCSYIFSHSMTKTLPGGIMVNGSRLKNLVLTYVN 300

Qy        301 AISSGDLPCIENAVLALAQRENSAAVQKAIAHYDQQMGQKVQLPMETLQELLDLHRTSER 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 AISSGDLPCIENAVLALAQRENSAAVQKAIAHYDQQMGQKVQLPMETLQELLDLHRTSER 360

Qy        361 EAIEVFMKNSFKDVDQSFQKELETLLDAKQNDICKRNLEASSDYCSALLKDIFGPLEEAV 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

```
Db        361 EAIEVFMKNSFKDVDQSFQKELETLLDAKQNDICKRNLEASSDYCSALLKDIFGPLEEAV 420

Qy        421 KQGIYSKPGGHNLFIQKTEELKAKYYREPRKGIQAEEVLQKYLKSKESVSHAILQTDQAL 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 KQGIYSKPGGHNLFIQKTEELKAKYYREPRKGIQAEEVLQKYLKSKESVSHAILQTDQAL 480

Qy        481 TETEKKKKEAQVKAEAEKAEAQRLAAIQRQNEQMMQERERLHQEQVRQMEIAKQNWLAEQ 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 TETEKKKKEAQVKAEAEKAEAQRLAAIQRQNEQMMQERERLHQEQVRQMEIAKQNWLAEQ 540

Qy        541 QKMQEQQMQ 549
              |||||||||
Db        541 QKMQEQQMQ 549


RESULT 12
ADA18646
ID   ADA18646 standard; protein; 586 AA.
XX
AC   ADA18646;
XX
DT   20-NOV-2003  (first entry)
XX
DE   Human PRO polypeptide #23.
XX
KW   Human; PRO; secreted polypeptide; transmembrane polypeptide;
KW   tumour necrosis factor-alpha; TNF-alpha; blood; chondrocyte cell; lung;
KW   colon; breast; prostate; rectum; cervix; liver; tumour; cancer;
KW   glucose uptake; FFA; adipocyte cell; pericyte cell; proteoglycan;
KW   cartilage; inner ear utricular supporting cell; cytokine; A-peptide;
KW   factor VIIA; endothelial cell.
XX
OS   Homo sapiens.
XX
PN   US2003054517-A1.
XX
PD   20-MAR-2003.
XX
PF   08-MAY-2002; 2002US-00141755.
XX
PR   31-MAR-1997;   97WO-US005230.
PR   12-JUN-1998;   98WO-US012456.
PR   14-JUL-1998;   98WO-US014552.
PR   28-AUG-1998;   98WO-US017888.
PR   10-SEP-1998;   98WO-US018824.
PR   14-SEP-1998;   98WO-US019093.
PR   14-SEP-1998;   98WO-US019094.
PR   14-SEP-1998;   98WO-US019177.
PR   16-SEP-1998;   98WO-US019330.
PR   17-SEP-1998;   98WO-US019437.
PR   07-OCT-1998;   98WO-US021141.
PR   29-OCT-1998;   98WO-US022991.
PR   29-OCT-1998;   98WO-US022992.
PR   20-NOV-1998;   98WO-US024855.
PR   01-DEC-1998;   98WO-US025108.
PR   05-JAN-1999;   99WO-US000106.
PR   08-MAR-1999;   99WO-US005028.
PR   10-MAR-1999;   99WO-US005190.
PR   20-APR-1999;   99WO-US008615.
PR   14-MAY-1999;   99WO-US010733.
PR   02-JUN-1999;   99WO-US012252.
PR   01-SEP-1999;   99WO-US020111.
PR   08-SEP-1999;   99WO-US020594.
PR   13-SEP-1999;   99WO-US020944.
PR   15-SEP-1999;   99WO-US021090.
PR   15-SEP-1999;   99WO-US021547.
PR   05-OCT-1999;   99WO-US023089.
PR   29-NOV-1999;   99WO-US028214.
PR   30-NOV-1999;   99WO-US028313.
PR   30-NOV-1999;   99WO-US028409.
PR   01-DEC-1999;   99WO-US028301.
PR   01-DEC-1999;   99WO-US028634.
PR   02-DEC-1999;   99WO-US028551.
PR   02-DEC-1999;   99WO-US028564.
PR   02-DEC-1999;   99WO-US028565.
PR   16-DEC-1999;   99WO-US030095.
PR   20-DEC-1999;   99WO-US030911.
PR   20-DEC-1999;   99WO-US030999.
PR   22-DEC-1999;   99WO-US030720.
PR   30-DEC-1999;   99WO-US031243.
PR   30-DEC-1999;   99WO-US031274.
PR   05-JAN-2000; 2000WO-US000219.
PR   06-JAN-2000; 2000WO-US000277.
PR   06-JAN-2000; 2000WO-US000376.
PR   11-FEB-2000; 2000WO-US003565.
PR   18-FEB-2000; 2000WO-US004341.
PR   18-FEB-2000; 2000WO-US004342.
PR   22-FEB-2000; 2000WO-US004414.
PR   24-FEB-2000; 2000WO-US004914.
PR   24-FEB-2000; 2000WO-US005004.
PR   01-MAR-2000; 2000WO-US005601.
PR   02-MAR-2000; 2000WO-US005746.
PR   02-MAR-2000; 2000WO-US005841.
PR   10-MAR-2000; 2000WO-US006319.
PR   15-MAR-2000; 2000WO-US006884.
PR   20-MAR-2000; 2000WO-US007377.
PR   21-MAR-2000; 2000WO-US007532.
PR   30-MAR-2000; 2000WO-US008439.
PR   17-MAY-2000; 2000WO-US013705.
PR   22-MAY-2000; 2000WO-US014042.
PR   30-MAY-2000; 2000WO-US014941.
PR   02-JUN-2000; 2000WO-US015264.
PR   28-JUL-2000; 2000WO-US020710.
PR   11-AUG-2000; 2000WO-US022031.
PR   23-AUG-2000; 2000WO-US023522.
PR   24-AUG-2000; 2000WO-US023328.
PR   08-NOV-2000; 2000WO-US030952.
PR   10-NOV-2000; 2000WO-US030873.
PR   01-DEC-2000; 2000WO-US032678.
PR   20-DEC-2000; 2000US-00747259.
PR   20-DEC-2000; 2000WO-US034956.
PR   28-FEB-2001; 2001US-00796498.
PR   28-FEB-2001; 2001WO-US006520.
PR   01-MAR-2001; 2001WO-US006666.
PR   09-MAR-2001; 2001US-00802706.
PR   14-MAR-2001; 2001US-00808689.
PR   22-MAR-2001; 2001US-00816744.
PR   05-APR-2001; 2001US-00828366.
PR   10-MAY-2001; 2001US-00854208.
PR   10-MAY-2001; 2001US-00854280.
PR   18-MAY-2001; 2001US-00860216.
PR   25-MAY-2001; 2001US-00866028.
PR   25-MAY-2001; 2001US-00866034.
PR   25-MAY-2001; 2001WO-US017092.
PR   01-JUN-2001; 2001US-00872035.
PR   01-JUN-2001; 2001WO-US017800.
PR   05-JUN-2001; 2001US-00874503.
PR   14-JUN-2001; 2001US-00882636.
PR   19-JUN-2001; 2001US-00886342.
PR   20-JUN-2001; 2001WO-US019692.
PR   21-JUN-2001; 2001US-00887879.
PR   22-JUN-2001; 2001WO-US020116.
PR   29-JUN-2001; 2001WO-US021066.
PR   09-JUL-2001; 2001WO-US021735.
PR   18-JUL-2001; 2001US-00908827.
PR   06-AUG-2001; 2001US-00924419.
PR   09-AUG-2001; 2001US-00927796.
PR   16-AUG-2001; 2001US-00931836.
PR   19-DEC-2001; 2001US-00028072.
XX
PA   (GETH ) GENENTECH INC.
XX
PI   Baker KP,  Beresini M,  Deforge L,  Desnoyers L,  Filvaroff E,  Gao W;
PI   Gerritsen ME,  Goddard A,  Godowski PJ,  Gurney AL,  Sherwood S;
PI   Smith V,  Stewart TA,  Tumas D,  Watanabe CK,  Wood WI,  Zhang Z;
XX
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DR   WPI; 2003-521854/49.
DR   N-PSDB; ADA18645.
XX
PT   New PRO nucleic acid, useful for preparing a composition for treating
PT   e.g., tumors.
XX
PS   Claim 12; Fig 46; 660pp; English.
XX
CC   The invention relates to isolated human PRO polypeptides (secreted and
CC   transmembrane polypeptides) and the polynucleotides encoding them. The
CC   invention also relates to an antibody which specifically binds to a PRO
CC   polypeptide, a method for stimulating the release of tumour necrosis
CC   factor-alpha (TNF-alpha) from human blood, a method for stimulating the
CC   proliferation or differentiation of chondrocyte cells and a method for
CC   detecting the presence of a tumour in a mammal (e.g. lung, colon, breast,
CC   prostate, rectal, cervical and liver tumours). The polynucleotides are
CC   useful in molecular biology, including uses as hybridisation probes, in
CC   chromosome and gene mapping, in generating antisense RNA and DNA and in
CC   gene therapy. The polynucleotides may also be used in preparing PRO
CC   polypeptides by recombinant techniques and in generating either
CC   transgenic animals or knock-out animals which are useful in the
CC   development and screening of therapeutically useful reagents. The PRO
CC   polypeptides or antibodies are used in preparing a medicament for
CC   treating a condition responsive to the polypeptides or antibodies, such
CC   as tumours, for modulating the uptake of glucose or FFA by adipocyte
CC   cells, for stimulating the proliferation of or gene expression in
CC   pericyte cells, for stimulating the release of proteoglycans from
CC   cartilage, for stimulating the proliferation of inner ear utricular
CC   supporting cells, for stimulating the release of cytokines from PBMC
CC   cells, for inhibiting the binding of A-peptide to factor VIIA, for
CC   inhibiting the differentiation of adipocyte cells and for stimulating the
CC   proliferation of endothelial cells. This sequence represents a human PRO
CC   polypeptide of the invention. Note: The sequence data for this patent is
CC   also available in electronic format from USPTO at
CC   seqdata.uspto.gov/sequence.html.
XX
SQ   Sequence 586 AA;

  Query Match             92.5%;  Score 2815;  DB 6;  Length 586;
  Best Local Similarity   100.0%;  Pred. No. 1.2e-222;
  Matches  549;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MALEIHMSDPMCLIENFNEQLKVNQEALEILSAITQPVVVVAIVGLYRTGKSYLMNKLAG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MALEIHMSDPMCLIENFNEQLKVNQEALEILSAITQPVVVVAIVGLYRTGKSYLMNKLAG 60

Qy         61 KNKGFSVASTVQSHTKGIWIWCVPHPNWPNHTLVLLDTEGLGDVEKADNKNDIQIFALAL 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 KNKGFSVASTVQSHTKGIWIWCVPHPNWPNHTLVLLDTEGLGDVEKADNKNDIQIFALAL 120

Qy        121 LLSSTFVYNTVNKIDQGAIDLLHNVTELTDLLKARNSPDLDRVEDPADSASFFPDLVWTL 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 LLSSTFVYNTVNKIDQGAIDLLHNVTELTDLLKARNSPDLDRVEDPADSASFFPDLVWTL 180

Qy        181 RDFCLGLEIDGQLVTPDEYLENSLRPKQGSDQRVQNFNLPRLCIQKFFPKKKCFIFDLPA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 RDFCLGLEIDGQLVTPDEYLENSLRPKQGSDQRVQNFNLPRLCIQKFFPKKKCFIFDLPA 240

Qy        241 HQKKLAQLETLPDDELEPEFVQQVTEFCSYIFSHSMTKTLPGGIMVNGSRLKNLVLTYVN 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 HQKKLAQLETLPDDELEPEFVQQVTEFCSYIFSHSMTKTLPGGIMVNGSRLKNLVLTYVN 300

Qy        301 AISSGDLPCIENAVLALAQRENSAAVQKAIAHYDQQMGQKVQLPMETLQELLDLHRTSER 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 AISSGDLPCIENAVLALAQRENSAAVQKAIAHYDQQMGQKVQLPMETLQELLDLHRTSER 360

Qy        361 EAIEVFMKNSFKDVDQSFQKELETLLDAKQNDICKRNLEASSDYCSALLKDIFGPLEEAV 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 EAIEVFMKNSFKDVDQSFQKELETLLDAKQNDICKRNLEASSDYCSALLKDIFGPLEEAV 420

Qy        421 KQGIYSKPGGHNLFIQKTEELKAKYYREPRKGIQAEEVLQKYLKSKESVSHAILQTDQAL 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 KQGIYSKPGGHNLFIQKTEELKAKYYREPRKGIQAEEVLQKYLKSKESVSHAILQTDQAL 480

Qy        481 TETEKKKKEAQVKAEAEKAEAQRLAAIQRQNEQMMQERERLHQEQVRQMEIAKQNWLAEQ 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 TETEKKKKEAQVKAEAEKAEAQRLAAIQRQNEQMMQERERLHQEQVRQMEIAKQNWLAEQ 540

Qy        541 QKMQEQQMQ 549
              |||||||||
Db        541 QKMQEQQMQ 549


RESULT 13
ADA61269
ID   ADA61269 standard; protein; 586 AA.
XX
AC   ADA61269;
XX
DT   20-NOV-2003  (first entry)
XX
DE   Homo sapiens.
XX
KW   Human; secreted and transmembrane protein; PRO;
KW   Tumour necrosis factor alpha release; TNF-alpha release;
KW   glucose uptake modulator; FFA uptake modulator;
KW   cell proliferation stimulator; cell differentiation stimulator;
KW   cell differentiation inihibitor; cytokine release stimulator; tumour;
KW   lung tumoue; colon tumour; breast tumour; prostate tumour; rectal tumour;
KW   cervical tumour; liver tumour; chromosome mapping; gene mapping;
KW   gene therapy; chromosome identification; chromosome marker.
XX
OS   Novel.
OS   human.
OS   secreted.
OS   and.
OS   transmembrane.
OS   protein.
OS   PRO4987.
XX
PN   US2003049816-A1.
XX
PD   13-MAR-2003.
XX
PF   15-APR-2002; 2002US-00123262.
XX
PR   31-MAR-1997;   97WO-US005230.
PR   12-JUN-1998;   98WO-US012456.
PR   14-JUL-1998;   98WO-US014552.
PR   28-AUG-1998;   98WO-US017888.
PR   10-SEP-1998;   98WO-US018824.
PR   14-SEP-1998;   98WO-US019093.
PR   14-SEP-1998;   98WO-US019094.
PR   14-SEP-1998;   98WO-US019177.
PR   16-SEP-1998;   98WO-US019330.
PR   17-SEP-1998;   98WO-US019437.
PR   07-OCT-1998;   98WO-US021141.
PR   29-OCT-1998;   98WO-US022991.
PR   29-OCT-1998;   98WO-US022992.
PR   20-NOV-1998;   98WO-US024855.
PR   01-DEC-1998;   98WO-US025108.
PR   05-JAN-1999;   99WO-US000106.
PR   08-MAR-1999;   99WO-US005028.
PR   10-MAR-1999;   99WO-US005190.
PR   20-APR-1999;   99WO-US008615.
PR   14-MAY-1999;   99WO-US010733.
PR   02-JUN-1999;   99WO-US012252.
PR   01-SEP-1999;   99WO-US020111.
PR   08-SEP-1999;   99WO-US020594.
PR   13-SEP-1999;   99WO-US020944.
PR   15-SEP-1999;   99WO-US021090.
PR   15-SEP-1999;   99WO-US021547.
PR   05-OCT-1999;   99WO-US023089.
PR   29-NOV-1999;   99WO-US028214.
PR   30-NOV-1999;   99WO-US028313.
PR   30-NOV-1999;   99WO-US028409.
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PR 01-DEC-1999; 99WO-US028301.
PR 01-DEC-1999; 99WO-US028634.
PR 02-DEC-1999; 99WO-US028551.
PR 02-DEC-1999; 99WO-US028564.
PR 02-DEC-1999; 99WO-US028565.
PR 16-DEC-1999; 99WO-US030095.
PR 20-DEC-1999; 99WO-US030911.
PR 20-DEC-1999; 99WO-US030999.
PR 22-DEC-1999; 99WO-US030720.
PR 30-DEC-1999; 99WO-US031243.
PR 30-DEC-1999; 99WO-US031274.
PR 05-JAN-2000; 2000WO-US000219.
PR 06-JAN-2000; 2000WO-US000277.
PR 06-JAN-2000; 2000WO-US000376.
PR 11-FEB-2000; 2000WO-US003565.
PR 18-FEB-2000; 2000WO-US004341.
PR 18-FEB-2000; 2000WO-US004342.
PR 22-FEB-2000; 2000WO-US004414.
PR 24-FEB-2000; 2000WO-US004914.
PR 24-FEB-2000; 2000WO-US005004.
PR 01-MAR-2000; 2000WO-US005601.
PR 02-MAR-2000; 2000WO-US005746.
PR 02-MAR-2000; 2000WO-US005841.
PR 10-MAR-2000; 2000WO-US006319.
PR 15-MAR-2000; 2000WO-US006884.
PR 20-MAR-2000; 2000WO-US007377.
PR 21-MAR-2000; 2000WO-US007532.
PR 30-MAR-2000; 2000WO-US008439.
PR 17-MAY-2000; 2000WO-US013705.
PR 22-MAY-2000; 2000WO-US014042.
PR 30-MAY-2000; 2000WO-US014941.
PR 02-JUN-2000; 2000WO-US015264.
PR 28-JUL-2000; 2000WO-US020710.
PR 11-AUG-2000; 2000WO-US022031.
PR 23-AUG-2000; 2000WO-US023522.
PR 24-AUG-2000; 2000WO-US023328.
PR 08-NOV-2000; 2000WO-US030952.
PR 10-NOV-2000; 2000WO-US030873.
PR 01-DEC-2000; 2000WO-US032678.
PR 20-DEC-2000; 2000US-00747259.
PR 20-DEC-2000; 2000WO-US034956.
PR 28-FEB-2001; 2001US-00796498.
PR 28-FEB-2001; 2001WO-US006520.
PR 01-MAR-2001; 2001WO-US006666.
PR 09-MAR-2001; 2001US-00802706.
PR 14-MAR-2001; 2001US-00808689.
PR 22-MAR-2001; 2001US-00816744.
PR 05-APR-2001; 2001US-00828366.
PR 10-MAY-2001; 2001US-00854208.
PR 10-MAY-2001; 2001US-00854280.
PR 18-MAY-2001; 2001US-00860216.
PR 25-MAY-2001; 2001US-00866028.
PR 25-MAY-2001; 2001US-00866034.
PR 25-MAY-2001; 2001WO-US017092.
PR 01-JUN-2001; 2001US-00872035.
PR 01-JUN-2001; 2001WO-US017800.
PR 05-JUN-2001; 2001US-00874503.
PR 14-JUN-2001; 2001US-00882636.
PR 19-JUN-2001; 2001US-00886342.
PR 20-JUN-2001; 2001WO-US019692.
PR 21-JUN-2001; 2001US-00887879.
PR 22-JUN-2001; 2001WO-US020116.
PR 29-JUN-2001; 2001WO-US021066.
PR 09-JUL-2001; 2001WO-US021735.
PR 18-JUL-2001; 2001US-00908827.
PR 06-AUG-2001; 2001US-00924419.
PR 09-AUG-2001; 2001US-00927796.
PR 16-AUG-2001; 2001US-00931836.
PR 19-DEC-2001; 2001US-00028072.
XX
PA (GETH) GENENTECH INC.
XX
PI Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, Gao W;
PI Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;
PI Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;
XX
DR WPI; 2003-695892/66.
DR N-PSDB; ADA61268.
XX
PT New PRO nucleic acid and encode polypeptides, are useful for
PT manufacturing a medicament for diagnosing or treating cancer.
XX
PS Claim 12; Fig 46; 660pp; English.
XX
CC The invention describes 305 nucleic acids encoding PRO (secreted and
CC transmembrane) polypeptides (I). (I) is useful for stimulating the
CC release of TNF-alpha from human blood, for modulating the uptake of
CC glucose or FFA by skeletal muscle cells or adipocyte cells, for
CC stimulating the proliferation or differentiation of chondrocyte cells,
CC for stimulating the proliferation of or gene expression in pericyte
CC cells, for stimulating the release of proteoglycans from cartilage, for
CC stimulating the proliferation of inner ear utricular supporting cells,
CC for stimulating the proliferation of T-lymphocyte cells, for stimulating
CC the release of a cytokine from PBMC cells, for inhibiting the binding of
CC A-peptide to factor VIIA, for inhibiting the differentiation of adipocyte
CC cells, for stimulating proliferation of endothelial cells, for detecting
CC the presence of tumour in a mammal. The tumour is lung, colon, breast,
CC prostate, rectal, cervical or liver tumour. The oligonucleotide probes
CC are useful for isolating genomic and cDNA nucleotide sequences or
CC antisense probes. (I) is also useful as therapeutic agent. PRO is useful
CC in assays to identify other proteins or molecules involved in binding
CC interaction. A polynucleotide (II) encoding (I) is useful in chromosome
CC and gene mapping, in generation of antisense RNA and DNA, in the
CC preparation of PRO polypeptide, for generating transgenic animals or
CC knockout animals which in turn are useful in the development and
CC screening of therapeutically useful reagents, in gene therapy, for
CC chromosome identification, as chromosome marker, and for generating
CC probes. An anti-(I)-antibody is useful in diagnostic assays for PRO, e.g.
CC detecting its expression in specific cells, tissues or serum, and for
CC affinity purification of PRO from recombinant cell culture or natural
CC sources. (I) and (II) are useful for tissue typing. This is the amino
CC acid sequence of a novel human secreted and transmembrane PRO
CC polypeptide.
XX
SQ Sequence 586 AA;

Query Match 92.5%; Score 2815; DB 6; Length 586;
Best Local Similarity 100.0%; Pred. No. 1.2e-222;
Matches 549; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 MALEIHMSDPMCLIENFNEQLKVNQEALEILSAITQPVVVVAIVGLYRTGKSYLMNKLAG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MALEIHMSDPMCLIENFNEQLKVNQEALEILSAITQPVVVVAIVGLYRTGKSYLMNKLAG 60

Qy         61 KNKGFSVASTVQSHTKGIWIWCVPHPNWPNHTLVLLDTEGLGDVEKADNKNDIQIFALAL 120
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Db         61 KNKGFSVASTVQSHTKGIWIWCVPHPNWPNHTLVLLDTEGLGDVEKADNKNDIQIFALAL 120

Qy        121 LLSSTFVYNTVNKIDQGAIDLLHNVTELTDLLKARNSPDLDRVEDPADSASFFPDLVWTL 180
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Db        121 LLSSTFVYNTVNKIDQGAIDLLHNVTELTDLLKARNSPDLDRVEDPADSASFFPDLVWTL 180

Qy        181 RDFCLGLEIDGQLVTPDEYLENSLRPKQGSDQRVQNFNLPRLCIQKFFPKKKCFIFDLPA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 RDFCLGLEIDGQLVTPDEYLENSLRPKQGSDQRVQNFNLPRLCIQKFFPKKKCFIFDLPA 240

Qy        241 HQKKLAQLETLPDDELEPEFVQQVTEFCSYIFSHSMTKTLPGGIMVNGSRLKNLVLTYVN 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 HQKKLAQLETLPDDELEPEFVQQVTEFCSYIFSHSMTKTLPGGIMVNGSRLKNLVLTYVN 300

Qy        301 AISSGDLPCIENAVLALAQRENSAAVQKAIAHYDQQMGQKVQLPMETLQELLDLHRTSER 360
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Db        301 AISSGDLPCIENAVLALAQRENSAAVQKAIAHYDQQMGQKVQLPMETLQELLDLHRTSER 360

Qy        361 EAIEVFMKNSFKDVDQSFQKELETLLDAKQNDICKRNLEASSDYCSALLKDIFGPLEEAV 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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```
Db        361 EAIEVFMKNSFKDVDQSFQKELETLLDAKQNDICKRNLEASSDYCSALLKDIFGPLEEAV 420

Qy        421 KQGIYSKPGGHNLFIQKTEELKAKYYREPRKGIQAEEVLQKYLKSKESVSHAILQTDQAL 480
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Db        421 KQGIYSKPGGHNLFIQKTEELKAKYYREPRKGIQAEEVLQKYLKSKESVSHAILQTDQAL 480

Qy        481 TETEKKKKEAQVKAEAEKAEAQRLAAIQRQNEQMMQERERLHQEQVRQMEIAKQNWLAEQ 540
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Db        481 TETEKKKKEAQVKAEAEKAEAQRLAAIQRQNEQMMQERERLHQEQVRQMEIAKQNWLAEQ 540

Qy        541 QKMQEQQMQ 549
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Db        541 QKMQEQQMQ 549


RESULT 14
ADB19054
ID   ADB19054 standard; protein; 586 AA.
XX
AC   ADB19054;
XX
DT   20-NOV-2003  (first entry)
XX
DE   Novel human secreted and transmembrane protein PRO4987.
XX
KW   Human; secreted and transmembrane protein; PRO;
KW   Tumour necrosis factor alpha release; TNF-alpha release;
KW   glucose uptake modulator; FFA uptake modulator;
KW   cell proliferation stimulator; cell differentiation stimulator;
KW   cell differentiation inihibitor; cytokine releas.
XX
OS   Homo sapiens.
XX
PN   US2003068796-A1.
XX
PD   10-APR-2003.
XX
PF   15-APR-2002; 2002US-00123261.
XX
PR   31-MAR-1997;   97WO-US005230.
PR   12-JUN-1998;   98WO-US012456.
PR   14-JUL-1998;   98WO-US014552.
PR   28-AUG-1998;   98WO-US017888.
PR   10-SEP-1998;   98WO-US018824.
PR   14-SEP-1998;   98WO-US019093.
PR   14-SEP-1998;   98WO-US019094.
PR   14-SEP-1998;   98WO-US019177.
PR   16-SEP-1998;   98WO-US019330.
PR   17-SEP-1998;   98WO-US019437.
PR   07-OCT-1998;   98WO-US021141.
PR   29-OCT-1998;   98WO-US022991.
PR   29-OCT-1998;   98WO-US022992.
PR   20-NOV-1998;   98WO-US024855.
PR   01-DEC-1998;   98WO-US025108.
PR   05-JAN-1999;   99WO-US000106.
PR   08-MAR-1999;   99WO-US005028.
PR   10-MAR-1999;   99WO-US005190.
PR   20-APR-1999;   99WO-US008615.
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PR   02-JUN-1999;   99WO-US012252.
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PR   05-JAN-2000; 2000WO-US000219.
PR   06-JAN-2000; 2000WO-US000277.
PR   06-JAN-2000; 2000WO-US000376.
PR   11-FEB-2000; 2000WO-US003565.
PR   18-FEB-2000; 2000WO-US004341.
PR   18-FEB-2000; 2000WO-US004342.
PR   22-FEB-2000; 2000WO-US004414.
PR   24-FEB-2000; 2000WO-US004914.
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PR   10-MAR-2000; 2000WO-US006319.
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PR   23-AUG-2000; 2000WO-US023522.
PR   24-AUG-2000; 2000WO-US023328.
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PR   10-NOV-2000; 2000WO-US030873.
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PR   20-DEC-2000; 2000US-00747259.
PR   20-DEC-2000; 2000WO-US034956.
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PR   01-MAR-2001; 2001WO-US006666.
PR   09-MAR-2001; 2001US-00802706.
PR   14-MAR-2001; 2001US-00808689.
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PR   10-MAY-2001; 2001US-00854208.
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PR   25-MAY-2001; 2001US-00866028.
PR   25-MAY-2001; 2001US-00866034.
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PR   01-JUN-2001; 2001US-00872035.
PR   01-JUN-2001; 2001WO-US017800.
PR   05-JUN-2001; 2001US-00874503.
PR   14-JUN-2001; 2001US-00882636.
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PR   06-AUG-2001; 2001US-00924419.
PR   09-AUG-2001; 2001US-00927796.
PR   16-AUG-2001; 2001US-00931836.
PR   19-DEC-2001; 2001US-00028072.
XX
PA   (GETH ) GENENTECH INC.
XX
PI   Baker KP,  Beresini M,  Deforge L,  Desnoyers L,  Filvaroff E,  Gao W;
PI   Gerritsen ME,  Goddard A,  Godowski PJ,  Gurney AL,  Sherwood S;
PI   Smith V,  Stewart TA,  Tumas D,  Watanabe CK,  Wood WI,  Zhang Z;
XX
DR   WPI; 2003-695927/66.
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DR   N-PSDB; ADB19053.
XX
PT   Novel secreted and transmembrane PRO polypeptides useful for stimulating
PT   the release of tumor necrosis factor alpha and detecting the presence of
PT   a tumor in a mammal.
XX
PS   Claim 12; Fig 46; 660pp; English.
XX
CC   The invention describes 305 nucleic acids encoding PRO (secreted and
CC   transmembrane) polypeptides (I). (I) is useful for stimulating the
CC   release of TNF-alpha from human blood, for modulating the uptake of
CC   glucose or FFA by skeletal muscle cells or adipocyt
XX
SQ   Sequence 586 AA;

  Query Match             92.5%;  Score 2815;  DB 6;  Length 586;
  Best Local Similarity   100.0%;  Pred. No. 1.2e-222;
  Matches  549;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Db         61 KNKGFSVASTVQSHTKGIWIWCVPHPNWPNHTLVLLDTEGLGDVEKADNKNDIQIFALAL 120

Qy        121 LLSSTFVYNTVNKIDQGAIDLLHNVTELTDLLKARNSPDLDRVEDPADSASFFPDLVWTL 180
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Db        121 LLSSTFVYNTVNKIDQGAIDLLHNVTELTDLLKARNSPDLDRVEDPADSASFFPDLVWTL 180

Qy        181 RDFCLGLEIDGQLVTPDEYLENSLRPKQGSDQRVQNFNLPRLCIQKFFPKKKCFIFDLPA 240
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Db        181 RDFCLGLEIDGQLVTPDEYLENSLRPKQGSDQRVQNFNLPRLCIQKFFPKKKCFIFDLPA 240

Qy        241 HQKKLAQLETLPDDELEPEFVQQVTEFCSYIFSHSMTKTLPGGIMVNGSRLKNLVLTYVN 300
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Db        241 HQKKLAQLETLPDDELEPEFVQQVTEFCSYIFSHSMTKTLPGGIMVNGSRLKNLVLTYVN 300

Qy        301 AISSGDLPCIENAVLALAQRENSAAVQKAIAHYDQQMGQKVQLPMETLQELLDLHRTSER 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 AISSGDLPCIENAVLALAQRENSAAVQKAIAHYDQQMGQKVQLPMETLQELLDLHRTSER 360

Qy        361 EAIEVFMKNSFKDVDQSFQKELETLLDAKQNDICKRNLEASSDYCSALLKDIFGPLEEAV 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 EAIEVFMKNSFKDVDQSFQKELETLLDAKQNDICKRNLEASSDYCSALLKDIFGPLEEAV 420

Qy        421 KQGIYSKPGGHNLFIQKTEELKAKYYREPRKGIQAEEVLQKYLKSKESVSHAILQTDQAL 480
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Db        421 KQGIYSKPGGHNLFIQKTEELKAKYYREPRKGIQAEEVLQKYLKSKESVSHAILQTDQAL 480

Qy        481 TETEKKKKEAQVKAEAEKAEAQRLAAIQRQNEQMMQERERLHQEQVRQMEIAKQNWLAEQ 540
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Db        481 TETEKKKKEAQVKAEAEKAEAQRLAAIQRQNEQMMQERERLHQEQVRQMEIAKQNWLAEQ 540

Qy        541 QKMQEQQMQ 549
              |||||||||
Db        541 QKMQEQQMQ 549


RESULT 15
ADB27595
ID   ADB27595 standard; protein; 586 AA.
XX
AC   ADB27595;
XX
DT   20-NOV-2003  (first entry)
XX
DE   Human PRO polypeptide #23.
XX
KW   Human; PRO; secreted polypeptide; transmembrane polypeptide;
KW   tumour necrosis factor-alpha; TNF-alpha; chondrocyte cell; tumour;
KW   cancer; adrenal; lung; colon; breast; prostate; rectum; kidney; cervix;
KW   liver; microvascular endothelial cell; glucose; FFA;
KW   skeletal muscle cell; adipocyte cell; pericyte cell;
KW   inner ear utricular supporting cell; T-lymphocyte cell;
KW   endothelial cell tube formation; bone disorder; cartilage disorder;
KW   sports injury; proteoglycan; articular cartilage defect; osteoarthritis;
KW   rheumatoid arthritis; haemoglobin-associated disorder thalassaemia;
KW   immune system cell infiltration.
XX
OS   Homo sapiens.
XX
PN   US2003082704-A1.
XX
PD   01-MAY-2003.
XX
PF   24-APR-2002; 2002US-00131819.
XX
PR   09-DEC-1999;   99US-0170262P.
PR   01-DEC-2000; 2000WO-US032678.
PR   19-DEC-2001; 2001US-00028072.
XX
PA   (GETH ) GENENTECH INC.
XX
PI   Baker KP,  Beresini M,  Deforge L,  Desnoyers L,  Filvaroff E,  Gao W;
PI   Gerritsen ME,  Goddard A,  Godowski PJ,  Gurney AL,  Sherwood S;
PI   Smith V,  Stewart TA,  Tumas D,  Watanabe CK,  Wood WI,  Zhang Z;
XX
DR   WPI; 2003-765415/72.
DR   N-PSDB; ADB27594.
XX
PT   New PRO nucleic acid, useful for preparing a composition for treating
PT   e.g., tumor or for tissue typing.
XX
PS   Claim 12; Fig 46; 637pp; English.
XX
CC   The invention relates to isolated human PRO polypeptides (secreted and
CC   transmembrane polypeptides) and the polynucleotides encoding them. The
CC   invention also relates to an antibody which specifically binds to a PRO
CC   polypeptide, a method for stimulating the release of tumour necrosis
CC   factor-alpha (TNF-alpha) from human blood, a method for stimulating the
CC   proliferation or differentiation of chondrocyte cells and a method for
CC   detecting the presence of a tumour in a mammal (e.g. adrenal, lung,
CC   colon, breast, prostate, rectal, kidney, cervical and liver tumours). The
CC   polynucleotides are useful in molecular biology, including uses as
CC   hybridisation probes, in chromosome and gene mapping, in generating
CC   antisense RNA and DNA and in gene therapy. The polynucleotides may also
CC   be used in preparing PRO polypeptides by recombinant techniques and in
CC   generating either transgenic animals or knock-out animals which are
CC   useful in the development and screening of therapeutically useful
CC   reagents. The PRO polypeptides or antibodies are used in preparing a
CC   medicament for treating a condition responsive to the polypeptides or
CC   antibodies, such as tumours, for stimulating and inhibiting proliferation
CC   of human microvascular endothelial cells, for modulating the uptake of
CC   glucose or FFA by skeletal muscle cells or adipocyte cells, for
CC   stimulating differentiation of adipocyte cells, for stimulating
CC   proliferation of or gene expression in pericyte cells, for stimulating
CC   the proliferation of inner ear utricular supporting cells or T-lymphocyte
CC   cells, for inducing endothelial cell tube formation and for treating
CC   various bone and/or cartilage disorders such as sports injuries and
CC   arthritis. PRO polypeptides which stimulate the release of proteoglycans
CC   from cartilage are useful for treating sports-related joint problems,
CC   articular cartilage defects, osteoarthritis and rheumatoid arthritis. PRO
CC   polypeptides are also useful for treating various mammalian haemoglobin-
CC   associated disorders such as various thalassaemias and conditions which
CC   may benefit from enhanced local immune system cell infiltration. This
CC   sequence represents a human PRO polypeptide of the invention. Note: The
CC   sequence data for this patent is also available in electronic format from
CC   the USPTO website at seqdata.uspto.gov.
XX
SQ   Sequence 586 AA;

  Query Match             92.5%;  Score 2815;  DB 6;  Length 586;
  Best Local Similarity   100.0%;  Pred. No. 1.2e-222;
  Matches  549;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
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Qy          1 MALEIHMSDPMCLIENFNEQLKVNQEALEILSAITQPVVVVAIVGLYRTGKSYLMNKLAG 60
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Qy         61 KNKGFSVASTVQSHTKGIWIWCVPHPNWPNHTLVLLDTEGLGDVEKADNKNDIQIFALAL 120
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Db         61 KNKGFSVASTVQSHTKGIWIWCVPHPNWPNHTLVLLDTEGLGDVEKADNKNDIQIFALAL 120

Qy        121 LLSSTFVYNTVNKIDQGAIDLLHNVTELTDLLKARNSPDLDRVEDPADSASFFPDLVWTL 180
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Db        121 LLSSTFVYNTVNKIDQGAIDLLHNVTELTDLLKARNSPDLDRVEDPADSASFFPDLVWTL 180

Qy        181 RDFCLGLEIDGQLVTPDEYLENSLRPKQGSDQRVQNFNLPRLCIQKFFPKKKCFIFDLPA 240
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Db        181 RDFCLGLEIDGQLVTPDEYLENSLRPKQGSDQRVQNFNLPRLCIQKFFPKKKCFIFDLPA 240

Qy        241 HQKKLAQLETLPDDELEPEFVQQVTEFCSYIFSHSMTKTLPGGIMVNGSRLKNLVLTYVN 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 HQKKLAQLETLPDDELEPEFVQQVTEFCSYIFSHSMTKTLPGGIMVNGSRLKNLVLTYVN 300

Qy        301 AISSGDLPCIENAVLALAQRENSAAVQKAIAHYDQQMGQKVQLPMETLQELLDLHRTSER 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 AISSGDLPCIENAVLALAQRENSAAVQKAIAHYDQQMGQKVQLPMETLQELLDLHRTSER 360

Qy        361 EAIEVFMKNSFKDVDQSFQKELETLLDAKQNDICKRNLEASSDYCSALLKDIFGPLEEAV 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 EAIEVFMKNSFKDVDQSFQKELETLLDAKQNDICKRNLEASSDYCSALLKDIFGPLEEAV 420

Qy        421 KQGIYSKPGGHNLFIQKTEELKAKYYREPRKGIQAEEVLQKYLKSKESVSHAILQTDQAL 480
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Db        421 KQGIYSKPGGHNLFIQKTEELKAKYYREPRKGIQAEEVLQKYLKSKESVSHAILQTDQAL 480

Qy        481 TETEKKKKEAQVKAEAEKAEAQRLAAIQRQNEQMMQERERLHQEQVRQMEIAKQNWLAEQ 540
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Qy        541 QKMQEQQMQ 549
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GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: July 9, 2005, 13:25:55 ; Search time 162 Seconds
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Title: US-10-659-549-3
Perfect score: 3043
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Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1726216 seqs, 386330316 residues

Total number of hits satisfying chosen parameters: 1726216

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	2815	92.5	586	14	US-10-140-808-46	Sequence 46, Appl
4	2815	92.5	586	14	US-10-121-049-46	Sequence 46, Appl
5	2815	92.5	586	14	US-10-123-904-46	Sequence 46, Appl
6	2815	92.5	586	14	US-10-140-470-46	Sequence 46, Appl
7	2815	92.5	586	14	US-10-175-746-46	Sequence 46, Appl
8	2815	92.5	586	14	US-10-176-918-46	Sequence 46, Appl
9	2815	92.5	586	14	US-10-176-921-46	Sequence 46, Appl
10	2815	92.5	586	14	US-10-137-865-46	Sequence 46, Appl
11	2815	92.5	586	14	US-10-140-474-46	Sequence 46, Appl
12	2815	92.5	586	14	US-10-142-431-46	Sequence 46, Appl
13	2815	92.5	586	14	US-10-143-114-46	Sequence 46, Appl
14	2815	92.5	586	14	US-10-142-419-46	Sequence 46, Appl
15	2815	92.5	586	14	US-10-123-262-46	Sequence 46, Appl
16	2815	92.5	586	14	US-10-142-423-46	Sequence 46, Appl
17	2815	92.5	586	14	US-10-121-050-46	Sequence 46, Appl
18	2815	92.5	586	14	US-10-141-755-46	Sequence 46, Appl
19	2815	92.5	586	14	US-10-143-032-46	Sequence 46, Appl
20	2815	92.5	586	14	US-10-123-108-46	Sequence 46, Appl
21	2815	92.5	586	14	US-10-123-236-46	Sequence 46, Appl
22	2815	92.5	586	14	US-10-123-261-46	Sequence 46, Appl
23	2815	92.5	586	14	US-10-140-921-46	Sequence 46, Appl
24	2815	92.5	586	14	US-10-140-928-46	Sequence 46, Appl
25	2815	92.5	586	14	US-10-121-045-46	Sequence 46, Appl
26	2815	92.5	586	14	US-10-123-292-46	Sequence 46, Appl
27	2815	92.5	586	14	US-10-123-903-46	Sequence 46, Appl
28	2815	92.5	586	14	US-10-124-819-46	Sequence 46, Appl
29	2815	92.5	586	14	US-10-124-822-46	Sequence 46, Appl
30	2815	92.5	586	14	US-10-140-925-46	Sequence 46, Appl
31	2815	92.5	586	14	US-10-160-498-46	Sequence 46, Appl
32	2815	92.5	586	14	US-10-124-824-46	Sequence 46, Appl
33	2815	92.5	586	14	US-10-127-825A-46	Sequence 46, Appl
34	2815	92.5	586	14	US-10-127-829A-46	Sequence 46, Appl
35	2815	92.5	586	14	US-10-127-835A-46	Sequence 46, Appl
36	2815	92.5	586	14	US-10-127-839A-46	Sequence 46, Appl
37	2815	92.5	586	14	US-10-127-901A-46	Sequence 46, Appl
38	2815	92.5	586	14	US-10-128-693A-46	Sequence 46, Appl
39	2815	92.5	586	14	US-10-131-813A-46	Sequence 46, Appl
40	2815	92.5	586	14	US-10-131-818A-46	Sequence 46, Appl
41	2815	92.5	586	14	US-10-131-823A-46	Sequence 46, Appl
42	2815	92.5	586	14	US-10-131-824A-46	Sequence 46, Appl
43	2815	92.5	586	14	US-10-131-830A-46	Sequence 46, Appl
44	2815	92.5	586	14	US-10-131-837A-46	Sequence 46, Appl
45	2815	92.5	586	14	US-10-137-872A-46	Sequence 46, Appl

ALIGNMENTS

RESULT 1
US-10-659-549-3
; Sequence 3, Application US/10659549
; Publication No. US20040229307A1
; GENERAL INFORMATION:
; APPLICANT: Diane Pennica
; TITLE OF INVENTION: GUANYLATE-BINDING PROTEIN
; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/659,549
; FILING DATE: 10-Sep-2003
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/015,089A
; FILING DATE: 29-Jan-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Hasak, Janet E.
; REGISTRATION NUMBER: 28,616
; REFERENCE/DOCKET NUMBER: P1056
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1896
; TELEFAX: 650/952-9881

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;   INFORMATION FOR SEQ ID NO: 3:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 591 amino acids
;             TYPE: Amino Acid
;             TOPOLOGY: Linear
;        SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-10-659-549-3

  Query Match             100.0%;  Score 3043;  DB 16;  Length 591;
  Best Local Similarity   100.0%;  Pred. No. 2.3e-213;
  Matches  591;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MALEIHMSDPMCLIENFNEQLKVNQEALEILSAITQPVVVVAIVGLYRTGKSYLMNKLAG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MALEIHMSDPMCLIENFNEQLKVNQEALEILSAITQPVVVVAIVGLYRTGKSYLMNKLAG 60

Qy         61 KNKGFSVASTVQSHTKGIWIWCVPHPNWPNHTLVLLDTEGLGDVEKADNKNDIQIFALAL 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 KNKGFSVASTVQSHTKGIWIWCVPHPNWPNHTLVLLDTEGLGDVEKADNKNDIQIFALAL 120

Qy        121 LLSSTFVYNTVNKIDQGAIDLLHNVTELTDLLKARNSPDLDRVEDPADSASFFPDLVWTL 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 LLSSTFVYNTVNKIDQGAIDLLHNVTELTDLLKARNSPDLDRVEDPADSASFFPDLVWTL 180

Qy        181 RDFCLGLEIDGQLVTPDEYLENSLRPKQGSDQRVQNFNLPRLCIQKFFPKKKCFIFDLPA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 RDFCLGLEIDGQLVTPDEYLENSLRPKQGSDQRVQNFNLPRLCIQKFFPKKKCFIFDLPA 240

Qy        241 HQKKLAQLETLPDDELEPEFVQQVTEFCSYIFSHSMTKTLPGGIMVNGSRLKNLVLTYVN 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 HQKKLAQLETLPDDELEPEFVQQVTEFCSYIFSHSMTKTLPGGIMVNGSRLKNLVLTYVN 300

Qy        301 AISSGDLPCIENAVLALAQRENSAAVQKAIAHYDQQMGQKVQLPMETLQELLDLHRTSER 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 AISSGDLPCIENAVLALAQRENSAAVQKAIAHYDQQMGQKVQLPMETLQELLDLHRTSER 360

Qy        361 EAIEVFMKNSFKDVDQSFQKELETLLDAKQNDICKRNLEASSDYCSALLKDIFGPLEEAV 420
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Db        361 EAIEVFMKNSFKDVDQSFQKELETLLDAKQNDICKRNLEASSDYCSALLKDIFGPLEEAV 420

Qy        421 KQGIYSKPGGHNLFIQKTEELKAKYYREPRKGIQAEEVLQKYLKSKESVSHAILQTDQAL 480
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Db        421 KQGIYSKPGGHNLFIQKTEELKAKYYREPRKGIQAEEVLQKYLKSKESVSHAILQTDQAL 480

Qy        481 TETEKKKKEAQVKAEAEKAEAQRLAAIQRQNEQMMQERERLHQEQVRQMEIAKQNWLAEQ 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 TETEKKKKEAQVKAEAEKAEAQRLAAIQRQNEQMMQERERLHQEQVRQMEIAKQNWLAEQ 540

Qy        541 QKMQEQQMQVFINCFISPLPVTMRVCSSGKEGEAARSCGSQQGVWSQKVWV 591
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Db        541 QKMQEQQMQVFINCFISPLPVTMRVCSSGKEGEAARSCGSQQGVWSQKVWV 591


RESULT 2
US-10-028-072-46
; Sequence 46, Application US/10028072
; Publication No. US20030004311A1
; GENERAL INFORMATION:
;  APPLICANT: Baker,Kevin P.
;  APPLICANT:  Beresini,Maureen
;  APPLICANT:  DeForge,Laura
;  APPLICANT:  Desnoyers,Luc
;  APPLICANT:  Filvaroff,Ellen
;  APPLICANT:  Gao,Wei-Qiang
;  APPLICANT:  Gerritsen,Mary E.
;  APPLICANT:  Goddard,Audrey
;  APPLICANT:  Godowski,Paul J.
;  APPLICANT:  Gurney,Austin L.
;  APPLICANT:  Sherwood,Steven
;  APPLICANT:  Smith,Victoria
;  APPLICANT:  Stewart,Timothy A.
;  APPLICANT:  Tumas,Daniel
;  APPLICANT:  Watanabe,Colin K
;  APPLICANT:  Wood,William
;  APPLICANT:  Zhang
;  TITLE OF INVENTION:
;  FILE REFERENCE:
;  CURRENT APPLICATION NUMBER: US/10/028,072
;  CURRENT FILING DATE:  2001-12-19
;  PRIOR APPLICATION NUMBER: 60/049911
;  PRIOR FILING DATE: 1997-06-18
;  PRIOR APPLICATION NUMBER: 60/056974
;  PRIOR FILING DATE: 1997-08-26
;  PRIOR APPLICATION NUMBER: 60/059113
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;  PRIOR APPLICATION NUMBER: 60/059115
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;  PRIOR APPLICATION NUMBER: 60/059117
;  PRIOR FILING DATE: 1997-09-17
;  PRIOR APPLICATION NUMBER: 60/059122
;  PRIOR FILING DATE: 1997-09-17
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;  PRIOR FILING DATE: 1997-09-18
;  PRIOR APPLICATION NUMBER: 60/059352
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;  PRIOR APPLICATION NUMBER: 60/059588
;  PRIOR FILING DATE: 1997-09-19
;  PRIOR APPLICATION NUMBER: 60/059836
;  PRIOR FILING DATE: 1997-09-24
;  PRIOR APPLICATION NUMBER: 60/062250
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; PRIOR APPLICATION NUMBER: 60/082999
; PRIOR FILING DATE: 1998-04-24
; PRIOR APPLICATION NUMBER: 60/083322
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; PRIOR APPLICATION NUMBER: 60/083545
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; PRIOR APPLICATION NUMBER: 60/084600
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/084627
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; PRIOR APPLICATION NUMBER: 60/084637
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/085149
; PRIOR FILING DATE: 1998-05-12
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; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: 60/088810
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; PRIOR APPLICATION NUMBER: 60/089947
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; PRIOR APPLICATION NUMBER: 60/090349
; PRIOR FILING DATE: 1998-06-23
; PRIOR APPLICATION NUMBER: 60/090429
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090445
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090538
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090863
; PRIOR FILING DATE: 1998-06-26
; PRIOR APPLICATION NUMBER: 60/091360
; PRIOR FILING DATE: 1998-07-01
; PRIOR APPLICATION NUMBER: 60/091519
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07

Query Match 92.5%; Score 2815; DB 14; Length 586;
Best Local Similarity 100.0%; Pred. No. 9.9e-197;
Matches 549; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 MALEIHMSDPMCLIENFNEQLKVNQEALEILSAITQPVVVVAIVGLYRTGKSYLMNKLAG 60
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Db          1 MALEIHMSDPMCLIENFNEQLKVNQEALEILSAITQPVVVVAIVGLYRTGKSYLMNKLAG 60

Qy         61 KNKGFSVASTVQSHTKGIWIWCVPHPNWPNHTLVLLDTEGLGDVEKADNKNDIQIFALAL 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 KNKGFSVASTVQSHTKGIWIWCVPHPNWPNHTLVLLDTEGLGDVEKADNKNDIQIFALAL 120

Qy        121 LLSSTFVYNTVNKIDQGAIDLLHNVTELTDLLKARNSPDLDRVEDPADSASFFPDLVWTL 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 LLSSTFVYNTVNKIDQGAIDLLHNVTELTDLLKARNSPDLDRVEDPADSASFFPDLVWTL 180

Qy        181 RDFCLGLEIDGQLVTPDEYLENSLRPKQGSDQRVQNFNLPRLCIQKFFPKKKCFIFDLPA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 RDFCLGLEIDGQLVTPDEYLENSLRPKQGSDQRVQNFNLPRLCIQKFFPKKKCFIFDLPA 240

Qy        241 HQKKLAQLETLPDDELEPEFVQQVTEFCSYIFSHSMTKTLPGGIMVNGSRLKNLVLTYVN 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 HQKKLAQLETLPDDELEPEFVQQVTEFCSYIFSHSMTKTLPGGIMVNGSRLKNLVLTYVN 300

Qy        301 AISSGDLPCIENAVLALAQRENSAAVQKAIAHYDQQMGQKVQLPMETLQELLDLHRTSER 360
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Db        301 AISSGDLPCIENAVLALAQRENSAAVQKAIAHYDQQMGQKVQLPMETLQELLDLHRTSER 360

Qy        361 EAIEVFMKNSFKDVDQSFQKELETLLDAKQNDICKRNLEASSDYCSALLKDIFGPLEEAV 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 EAIEVFMKNSFKDVDQSFQKELETLLDAKQNDICKRNLEASSDYCSALLKDIFGPLEEAV 420

Qy        421 KQGIYSKPGGHNLFIQKTEELKAKYYREPRKGIQAEEVLQKYLKSKESVSHAILQTDQAL 480
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Qy        481 TETEKKKKEAQVKAEAEKAEAQRLAAIQRQNEQMMQERERLHQEQVRQMEIAKQNWLAEQ 540
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Qy        541 QKMQEQQMQ 549
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RESULT 3
US-10-140-808-46
; Sequence 46, Application US/10140808
; Publication No. US20030017563A1
; GENERAL INFORMATION:
;  APPLICANT: Baker,Kevin P.
;  APPLICANT:  Beresini,Maureen
;  APPLICANT:  DeForge,Laura
;  APPLICANT:  Desnoyers,Luc
;  APPLICANT:  Filvaroff,Ellen
;  APPLICANT:  Gao,Wei-Qiang
;  APPLICANT:  Gerritsen,Mary E.
;  APPLICANT:  Goddard,Audrey
;  APPLICANT:  Godowski,Paul J.
;  APPLICANT:  Gurney,Austin L.
;  APPLICANT:  Sherwood,Steven
;  APPLICANT:  Smith,Victoria
;  APPLICANT:  Stewart,Timothy A.
;  APPLICANT:  Tumas,Daniel
;  APPLICANT:  Watanabe,Colin K
;  APPLICANT:  Wood,William
;  APPLICANT:  Zhang, Zemin
;  TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
;  TITLE OF INVENTION:  ACIDS ENCODING THE SAME
;  FILE REFERENCE: P3330R1C182
;  CURRENT APPLICATION NUMBER: US/10/140,808
;  CURRENT FILING DATE:  2002-05-07
;  Prior Apploication removed - See File Wrapper or Palm
;  NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 46
;   LENGTH: 586
;   TYPE: PRT
;   ORGANISM: Homo Sapien
US-10-140-808-46

  Query Match             92.5%;  Score 2815;  DB 14;  Length 586;
  Best Local Similarity   100.0%;  Pred. No. 9.9e-197;
  Matches  549;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MALEIHMSDPMCLIENFNEQLKVNQEALEILSAITQPVVVVAIVGLYRTGKSYLMNKLAG 60
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Db          1 MALEIHMSDPMCLIENFNEQLKVNQEALEILSAITQPVVVVAIVGLYRTGKSYLMNKLAG 60

Qy         61 KNKGFSVASTVQSHTKGIWIWCVPHPNWPNHTLVLLDTEGLGDVEKADNKNDIQIFALAL 120
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Db         61 KNKGFSVASTVQSHTKGIWIWCVPHPNWPNHTLVLLDTEGLGDVEKADNKNDIQIFALAL 120

Qy        121 LLSSTFVYNTVNKIDQGAIDLLHNVTELTDLLKARNSPDLDRVEDPADSASFFPDLVWTL 180
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Db        121 LLSSTFVYNTVNKIDQGAIDLLHNVTELTDLLKARNSPDLDRVEDPADSASFFPDLVWTL 180

Qy        181 RDFCLGLEIDGQLVTPDEYLENSLRPKQGSDQRVQNFNLPRLCIQKFFPKKKCFIFDLPA 240
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Db        181 RDFCLGLEIDGQLVTPDEYLENSLRPKQGSDQRVQNFNLPRLCIQKFFPKKKCFIFDLPA 240

Qy        241 HQKKLAQLETLPDDELEPEFVQQVTEFCSYIFSHSMTKTLPGGIMVNGSRLKNLVLTYVN 300
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Db        241 HQKKLAQLETLPDDELEPEFVQQVTEFCSYIFSHSMTKTLPGGIMVNGSRLKNLVLTYVN 300

Qy        301 AISSGDLPCIENAVLALAQRENSAAVQKAIAHYDQQMGQKVQLPMETLQELLDLHRTSER 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 AISSGDLPCIENAVLALAQRENSAAVQKAIAHYDQQMGQKVQLPMETLQELLDLHRTSER 360

Qy        361 EAIEVFMKNSFKDVDQSFQKELETLLDAKQNDICKRNLEASSDYCSALLKDIFGPLEEAV 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 EAIEVFMKNSFKDVDQSFQKELETLLDAKQNDICKRNLEASSDYCSALLKDIFGPLEEAV 420

Qy        421 KQGIYSKPGGHNLFIQKTEELKAKYYREPRKGIQAEEVLQKYLKSKESVSHAILQTDQAL 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 KQGIYSKPGGHNLFIQKTEELKAKYYREPRKGIQAEEVLQKYLKSKESVSHAILQTDQAL 480

Qy        481 TETEKKKKEAQVKAEAEKAEAQRLAAIQRQNEQMMQERERLHQEQVRQMEIAKQNWLAEQ 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 TETEKKKKEAQVKAEAEKAEAQRLAAIQRQNEQMMQERERLHQEQVRQMEIAKQNWLAEQ 540

Qy        541 QKMQEQQMQ 549
              |||||||||
Db        541 QKMQEQQMQ 549


RESULT 4
US-10-121-049-46
; Sequence 46, Application US/10121049
; Publication No. US20030022239A1
; GENERAL INFORMATION:
;  APPLICANT: Baker,Kevin P.
;  APPLICANT:  Beresini,Maureen
;  APPLICANT:  DeForge,Laura
;  APPLICANT:  Desnoyers,Luc
;  APPLICANT:  Filvaroff,Ellen
;  APPLICANT:  Gao,Wei-Qiang
;  APPLICANT:  Gerritsen,Mary E.
;  APPLICANT:  Goddard,Audrey
;  APPLICANT:  Godowski,Paul J.
;  APPLICANT:  Gurney,Austin L.
;  APPLICANT:  Sherwood,Steven
;  APPLICANT:  Smith,Victoria
;  APPLICANT:  Stewart,Timothy A.
;  APPLICANT:  Tumas,Daniel
;  APPLICANT:  Watanabe,Colin K
;  APPLICANT:  Wood,William
;  APPLICANT:  Zhang, Zemin
;  TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
;  TITLE OF INVENTION:  ACIDS ENCODING THE SAME
;  FILE REFERENCE: P3330R1C17
;  CURRENT APPLICATION NUMBER: US/10/121,049
;  CURRENT FILING DATE:  2002-04-12
;       Prior Application removed - See File Wrapper or Palm
;  NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 46
;   LENGTH: 586
;   TYPE: PRT
;   ORGANISM: Homo Sapien
US-10-121-049-46

  Query Match             92.5%;  Score 2815;  DB 14;  Length 586;
  Best Local Similarity   100.0%;  Pred. No. 9.9e-197;
  Matches  549;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MALEIHMSDPMCLIENFNEQLKVNQEALEILSAITQPVVVVAIVGLYRTGKSYLMNKLAG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MALEIHMSDPMCLIENFNEQLKVNQEALEILSAITQPVVVVAIVGLYRTGKSYLMNKLAG 60

Qy         61 KNKGFSVASTVQSHTKGIWIWCVPHPNWPNHTLVLLDTEGLGDVEKADNKNDIQIFALAL 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 KNKGFSVASTVQSHTKGIWIWCVPHPNWPNHTLVLLDTEGLGDVEKADNKNDIQIFALAL 120

Qy        121 LLSSTFVYNTVNKIDQGAIDLLHNVTELTDLLKARNSPDLDRVEDPADSASFFPDLVWTL 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 LLSSTFVYNTVNKIDQGAIDLLHNVTELTDLLKARNSPDLDRVEDPADSASFFPDLVWTL 180

Qy        181 RDFCLGLEIDGQLVTPDEYLENSLRPKQGSDQRVQNFNLPRLCIQKFFPKKKCFIFDLPA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 RDFCLGLEIDGQLVTPDEYLENSLRPKQGSDQRVQNFNLPRLCIQKFFPKKKCFIFDLPA 240

Qy        241 HQKKLAQLETLPDDELEPEFVQQVTEFCSYIFSHSMTKTLPGGIMVNGSRLKNLVLTYVN 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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```
Db        241 HQKKLAQLETLPDDELEPEFVQQVTEFCSYIFSHSMTKTLPGGIMVNGSRLKNLVLTYVN 300

Qy        301 AISSGDLPCIENAVLALAQRENSAAVQKAIAHYDQQMGQKVQLPMETLQELLDLHRTSER 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 AISSGDLPCIENAVLALAQRENSAAVQKAIAHYDQQMGQKVQLPMETLQELLDLHRTSER 360

Qy        361 EAIEVFMKNSFKDVDQSFQKELETLLDAKQNDICKRNLEASSDYCSALLKDIFGPLEEAV 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 EAIEVFMKNSFKDVDQSFQKELETLLDAKQNDICKRNLEASSDYCSALLKDIFGPLEEAV 420

Qy        421 KQGIYSKPGGHNLFIQKTEELKAKYYREPRKGIQAEEVLQKYLKSKESVSHAILQTDQAL 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 KQGIYSKPGGHNLFIQKTEELKAKYYREPRKGIQAEEVLQKYLKSKESVSHAILQTDQAL 480

Qy        481 TETEKKKKEAQVKAEAEKAEAQRLAAIQRQNEQMMQERERLHQEQVRQMEIAKQNWLAEQ 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 TETEKKKKEAQVKAEAEKAEAQRLAAIQRQNEQMMQERERLHQEQVRQMEIAKQNWLAEQ 540

Qy        541 QKMQEQQMQ 549
              |||||||||
Db        541 QKMQEQQMQ 549


RESULT 5
US-10-123-904-46
; Sequence 46, Application US/10123904
; Publication No. US20030022328A1
; GENERAL INFORMATION:
;  APPLICANT: Baker,Kevin P.
;  APPLICANT:  Beresini,Maureen
;  APPLICANT:  DeForge,Laura
;  APPLICANT:  Desnoyers,Luc
;  APPLICANT:  Filvaroff,Ellen
;  APPLICANT:  Gao,Wei-Qiang
;  APPLICANT:  Gerritsen,Mary E.
;  APPLICANT:  Goddard,Audrey
;  APPLICANT:  Godowski,Paul J.
;  APPLICANT:  Gurney,Austin L.
;  APPLICANT:  Sherwood,Steven
;  APPLICANT:  Smith,Victoria
;  APPLICANT:  Stewart,Timothy A.
;  APPLICANT:  Tumas,Daniel
;  APPLICANT:  Watanabe,Colin K
;  APPLICANT:  Wood,William
;  APPLICANT:  Zhang, Zemin
;  TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
;  TITLE OF INVENTION:  ACIDS ENCODING THE SAME
;  FILE REFERENCE: P3330R1C54
;  CURRENT APPLICATION NUMBER: US/10/123,904
;  CURRENT FILING DATE:  2002-04-16
;  Prior Application removed - See File Wrapper or Palm
;  NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 46
;   LENGTH: 586
;   TYPE: PRT
;   ORGANISM: Homo Sapien
US-10-123-904-46

  Query Match           92.5%;  Score 2815;  DB 14;  Length 586;
  Best Local Similarity  100.0%;  Pred. No. 9.9e-197;
  Matches  549;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MALEIHMSDPMCLIENFNEQLKVNQEALEILSAITQPVVVVAIVGLYRTGKSYLMNKLAG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MALEIHMSDPMCLIENFNEQLKVNQEALEILSAITQPVVVVAIVGLYRTGKSYLMNKLAG 60

Qy         61 KNKGFSVASTVQSHTKGIWIWCVPHPNWPNHTLVLLDTEGLGDVEKADNKNDIQIFALAL 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 KNKGFSVASTVQSHTKGIWIWCVPHPNWPNHTLVLLDTEGLGDVEKADNKNDIQIFALAL 120

Qy        121 LLSSTFVYNTVNKIDQGAIDLLHNVTELTDLLKARNSPDLDRVEDPADSASFFPDLVWTL 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 LLSSTFVYNTVNKIDQGAIDLLHNVTELTDLLKARNSPDLDRVEDPADSASFFPDLVWTL 180

Qy        181 RDFCLGLEIDGQLVTPDEYLENSLRPKQGSDQRVQNFNLPRLCIQKFFPKKKCFIFDLPA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 RDFCLGLEIDGQLVTPDEYLENSLRPKQGSDQRVQNFNLPRLCIQKFFPKKKCFIFDLPA 240

Qy        241 HQKKLAQLETLPDDELEPEFVQQVTEFCSYIFSHSMTKTLPGGIMVNGSRLKNLVLTYVN 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 HQKKLAQLETLPDDELEPEFVQQVTEFCSYIFSHSMTKTLPGGIMVNGSRLKNLVLTYVN 300

Qy        301 AISSGDLPCIENAVLALAQRENSAAVQKAIAHYDQQMGQKVQLPMETLQELLDLHRTSER 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 AISSGDLPCIENAVLALAQRENSAAVQKAIAHYDQQMGQKVQLPMETLQELLDLHRTSER 360

Qy        361 EAIEVFMKNSFKDVDQSFQKELETLLDAKQNDICKRNLEASSDYCSALLKDIFGPLEEAV 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 EAIEVFMKNSFKDVDQSFQKELETLLDAKQNDICKRNLEASSDYCSALLKDIFGPLEEAV 420

Qy        421 KQGIYSKPGGHNLFIQKTEELKAKYYREPRKGIQAEEVLQKYLKSKESVSHAILQTDQAL 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 KQGIYSKPGGHNLFIQKTEELKAKYYREPRKGIQAEEVLQKYLKSKESVSHAILQTDQAL 480

Qy        481 TETEKKKKEAQVKAEAEKAEAQRLAAIQRQNEQMMQERERLHQEQVRQMEIAKQNWLAEQ 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 TETEKKKKEAQVKAEAEKAEAQRLAAIQRQNEQMMQERERLHQEQVRQMEIAKQNWLAEQ 540

Qy        541 QKMQEQQMQ 549
              |||||||||
Db        541 QKMQEQQMQ 549


RESULT 6
US-10-140-470-46
; Sequence 46, Application US/10140470
; Publication No. US20030022331A1
; GENERAL INFORMATION:
;  APPLICANT: Baker,Kevin P.
;  APPLICANT:  Beresini,Maureen
;  APPLICANT:  DeForge,Laura
;  APPLICANT:  Desnoyers,Luc
;  APPLICANT:  Filvaroff,Ellen
;  APPLICANT:  Gao,Wei-Qiang
;  APPLICANT:  Gerritsen,Mary E.
;  APPLICANT:  Goddard,Audrey
;  APPLICANT:  Godowski,Paul J.
;  APPLICANT:  Gurney,Austin L.
;  APPLICANT:  Sherwood,Steven
;  APPLICANT:  Smith,Victoria
;  APPLICANT:  Stewart,Timothy A.
;  APPLICANT:  Tumas,Daniel
;  APPLICANT:  Watanabe,Colin K
;  APPLICANT:  Wood,William
;  APPLICANT:  Zhang, Zemin
;  TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
;  TITLE OF INVENTION:  ACIDS ENCODING THE SAME
;  FILE REFERENCE: P3330R1C160
;  CURRENT APPLICATION NUMBER: US/10/140,470
;  CURRENT FILING DATE:  2002-05-06
;  Prior Application removed - See Palm or File Wrapper
;  NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 46
;   LENGTH: 586
;   TYPE: PRT
;   ORGANISM: Homo Sapien
US-10-140-470-46

  Query Match           92.5%;  Score 2815;  DB 14;  Length 586;
  Best Local Similarity  100.0%;  Pred. No. 9.9e-197;
  Matches  549;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MALEIHMSDPMCLIENFNEQLKVNQEALEILSAITQPVVVVAIVGLYRTGKSYLMNKLAG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MALEIHMSDPMCLIENFNEQLKVNQEALEILSAITQPVVVVAIVGLYRTGKSYLMNKLAG 60
```

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Qy         61 KNKGFSVASTVQSHTKGIWIWCVPHPNWPNHTLVLLDTEGLGDVEKADNKNDIQIFALAL 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 KNKGFSVASTVQSHTKGIWIWCVPHPNWPNHTLVLLDTEGLGDVEKADNKNDIQIFALAL 120

Qy        121 LLSSTFVYNTVNKIDQGAIDLLHNVTELTDLLKARNSPDLDRVEDPADSASFFPDLVWTL 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 LLSSTFVYNTVNKIDQGAIDLLHNVTELTDLLKARNSPDLDRVEDPADSASFFPDLVWTL 180

Qy        181 RDFCLGLEIDGQLVTPDEYLENSLRPKQGSDQRVQNFNLPRLCIQKFFPKKKCFIFDLPA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 RDFCLGLEIDGQLVTPDEYLENSLRPKQGSDQRVQNFNLPRLCIQKFFPKKKCFIFDLPA 240

Qy        241 HQKKLAQLETLPDDELEPEFVQQVTEFCSYIFSHSMTKTLPGGIMVNGSRLKNLVLTYVN 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 HQKKLAQLETLPDDELEPEFVQQVTEFCSYIFSHSMTKTLPGGIMVNGSRLKNLVLTYVN 300

Qy        301 AISSGDLPCIENAVLALAQRENSAAVQKAIAHYDQQMGQKVQLPMETLQELLDLHRTSER 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 AISSGDLPCIENAVLALAQRENSAAVQKAIAHYDQQMGQKVQLPMETLQELLDLHRTSER 360

Qy        361 EAIEVFMKNSFKDVDQSFQKELETLLDAKQNDICKRNLEASSDYCSALLKDIFGPLEEAV 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 EAIEVFMKNSFKDVDQSFQKELETLLDAKQNDICKRNLEASSDYCSALLKDIFGPLEEAV 420

Qy        421 KQGIYSKPGGHNLFIQKTEELKAKYYREPRKGIQAEEVLQKYLKSKESVSHAILQTDQAL 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 KQGIYSKPGGHNLFIQKTEELKAKYYREPRKGIQAEEVLQKYLKSKESVSHAILQTDQAL 480

Qy        481 TETEKKKKEAQVKAEAEKAEAQRLAAIQRQNEQMMQERERLHQEQVRQMEIAKQNWLAEQ 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 TETEKKKKEAQVKAEAEKAEAQRLAAIQRQNEQMMQERERLHQEQVRQMEIAKQNWLAEQ 540

Qy        541 QKMQEQQMQ 549
              |||||||||
Db        541 QKMQEQQMQ 549
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RESULT 7
US-10-175-746-46
; Sequence 46, Application US/10175746
; Publication No. US20030027270A1
; GENERAL INFORMATION:
; APPLICANT: Baker,Kevin P.
; APPLICANT: Beresini,Maureen
; APPLICANT: DeForge,Laura
; APPLICANT: Desnoyers,Luc
; APPLICANT: Filvaroff,Ellen
; APPLICANT: Gao,Wei-Qiang
; APPLICANT: Gerritsen,Mary E.
; APPLICANT: Goddard,Audrey
; APPLICANT: Godowski,Paul J.
; APPLICANT: Gurney,Austin L.
; APPLICANT: Sherwood,Steven
; APPLICANT: Smith,Victoria
; APPLICANT: Stewart,Timothy A.
; APPLICANT: Tumas,Daniel
; APPLICANT: Watanabe,Colin K
; APPLICANT: Wood,William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3330R1C353
; CURRENT APPLICATION NUMBER: US/10/175,746
; CURRENT FILING DATE: 2002-06-19
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 46
; LENGTH: 586
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-175-746-46

Query Match 92.5%; Score 2815; DB 14; Length 586;

Best Local Similarity 100.0%; Pred. No. 9.9e-197;
Matches 549; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 MALEIHMSDPMCLIENFNEQLKVNQEALEILSAITQPVVVVAIVGLYRTGKSYLMNKLAG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MALEIHMSDPMCLIENFNEQLKVNQEALEILSAITQPVVVVAIVGLYRTGKSYLMNKLAG 60

Qy         61 KNKGFSVASTVQSHTKGIWIWCVPHPNWPNHTLVLLDTEGLGDVEKADNKNDIQIFALAL 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 KNKGFSVASTVQSHTKGIWIWCVPHPNWPNHTLVLLDTEGLGDVEKADNKNDIQIFALAL 120

Qy        121 LLSSTFVYNTVNKIDQGAIDLLHNVTELTDLLKARNSPDLDRVEDPADSASFFPDLVWTL 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 LLSSTFVYNTVNKIDQGAIDLLHNVTELTDLLKARNSPDLDRVEDPADSASFFPDLVWTL 180

Qy        181 RDFCLGLEIDGQLVTPDEYLENSLRPKQGSDQRVQNFNLPRLCIQKFFPKKKCFIFDLPA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 RDFCLGLEIDGQLVTPDEYLENSLRPKQGSDQRVQNFNLPRLCIQKFFPKKKCFIFDLPA 240

Qy        241 HQKKLAQLETLPDDELEPEFVQQVTEFCSYIFSHSMTKTLPGGIMVNGSRLKNLVLTYVN 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 HQKKLAQLETLPDDELEPEFVQQVTEFCSYIFSHSMTKTLPGGIMVNGSRLKNLVLTYVN 300

Qy        301 AISSGDLPCIENAVLALAQRENSAAVQKAIAHYDQQMGQKVQLPMETLQELLDLHRTSER 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 AISSGDLPCIENAVLALAQRENSAAVQKAIAHYDQQMGQKVQLPMETLQELLDLHRTSER 360

Qy        361 EAIEVFMKNSFKDVDQSFQKELETLLDAKQNDICKRNLEASSDYCSALLKDIFGPLEEAV 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 EAIEVFMKNSFKDVDQSFQKELETLLDAKQNDICKRNLEASSDYCSALLKDIFGPLEEAV 420

Qy        421 KQGIYSKPGGHNLFIQKTEELKAKYYREPRKGIQAEEVLQKYLKSKESVSHAILQTDQAL 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 KQGIYSKPGGHNLFIQKTEELKAKYYREPRKGIQAEEVLQKYLKSKESVSHAILQTDQAL 480

Qy        481 TETEKKKKEAQVKAEAEKAEAQRLAAIQRQNEQMMQERERLHQEQVRQMEIAKQNWLAEQ 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 TETEKKKKEAQVKAEAEKAEAQRLAAIQRQNEQMMQERERLHQEQVRQMEIAKQNWLAEQ 540

Qy        541 QKMQEQQMQ 549
              |||||||||
Db        541 QKMQEQQMQ 549
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RESULT 8
US-10-176-918-46
; Sequence 46, Application US/10176918
; Publication No. US20030027275A1
; GENERAL INFORMATION:
; APPLICANT: Baker,Kevin P.
; APPLICANT: Beresini,Maureen
; APPLICANT: DeForge,Laura
; APPLICANT: Desnoyers,Luc
; APPLICANT: Filvaroff,Ellen
; APPLICANT: Gao,Wei-Qiang
; APPLICANT: Gerritsen,Mary E.
; APPLICANT: Goddard,Audrey
; APPLICANT: Godowski,Paul J.
; APPLICANT: Gurney,Austin L.
; APPLICANT: Sherwood,Steven
; APPLICANT: Smith,Victoria
; APPLICANT: Stewart,Timothy A.
; APPLICANT: Tumas,Daniel
; APPLICANT: Watanabe,Colin K
; APPLICANT: Wood,William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3330R1C382
; CURRENT APPLICATION NUMBER: US/10/176,918
; CURRENT FILING DATE: 2002-06-20
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 550

```
; SEQ ID NO 46
;   LENGTH: 586
;   TYPE: PRT
;   ORGANISM: Homo Sapien
US-10-176-918-46

  Query Match             92.5%;  Score 2815;  DB 14;  Length 586;
  Best Local Similarity   100.0%;  Pred. No. 9.9e-197;
  Matches  549;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MALEIHMSDPMCLIENFNEQLKVNQEALEILSAITQPVVVVAIVGLYRTGKSYLMNKLAG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MALEIHMSDPMCLIENFNEQLKVNQEALEILSAITQPVVVVAIVGLYRTGKSYLMNKLAG 60

Qy         61 KNKGFSVASTVQSHTKGIWIWCVPHPNWPNHTLVLLDTEGLGDVEKADNKNDIQIFALAL 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 KNKGFSVASTVQSHTKGIWIWCVPHPNWPNHTLVLLDTEGLGDVEKADNKNDIQIFALAL 120

Qy        121 LLSSTFVYNTVNKIDQGAIDLLHNVTELTDLLKARNSPDLDRVEDPADSASFFPDLVWTL 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 LLSSTFVYNTVNKIDQGAIDLLHNVTELTDLLKARNSPDLDRVEDPADSASFFPDLVWTL 180

Qy        181 RDFCLGLEIDGQLVTPDEYLENSLRPKQGSDQRVQNFNLPRLCIQKFFPKKKCFIFDLPA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 RDFCLGLEIDGQLVTPDEYLENSLRPKQGSDQRVQNFNLPRLCIQKFFPKKKCFIFDLPA 240

Qy        241 HQKKLAQLETLPDDELEPEFVQQVTEFCSYIFSHSMTKTLPGGIMVNGSRLKNLVLTYVN 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 HQKKLAQLETLPDDELEPEFVQQVTEFCSYIFSHSMTKTLPGGIMVNGSRLKNLVLTYVN 300

Qy        301 AISSGDLPCIENAVLALAQRENSAAVQKAIAHYDQQMGQKVQLPMETLQELLDLHRTSER 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 AISSGDLPCIENAVLALAQRENSAAVQKAIAHYDQQMGQKVQLPMETLQELLDLHRTSER 360

Qy        361 EAIEVFMKNSFKDVDQSFQKELETLLDAKQNDICKRNLEASSDYCSALLKDIFGPLEEAV 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 EAIEVFMKNSFKDVDQSFQKELETLLDAKQNDICKRNLEASSDYCSALLKDIFGPLEEAV 420

Qy        421 KQGIYSKPGGHNLFIQKTEELKAKYYREPRKGIQAEEVLQKYLKSKESVSHAILQTDQAL 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 KQGIYSKPGGHNLFIQKTEELKAKYYREPRKGIQAEEVLQKYLKSKESVSHAILQTDQAL 480

Qy        481 TETEKKKKEAQVKAEAEKAEAQRLAAIQRQNEQMMQERERLHQEQVRQMEIAKQNWLAEQ 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 TETEKKKKEAQVKAEAEKAEAQRLAAIQRQNEQMMQERERLHQEQVRQMEIAKQNWLAEQ 540

Qy        541 QKMQEQQMQ 549
              |||||||||
Db        541 QKMQEQQMQ 549


RESULT 9
US-10-176-921-46
; Sequence 46, Application US/10176921
; Publication No. US20030027276A1
; GENERAL INFORMATION:
;  APPLICANT: Baker,Kevin P.
;  APPLICANT:  Beresini,Maureen
;  APPLICANT:  DeForge,Laura
;  APPLICANT:  Desnoyers,Luc
;  APPLICANT:  Filvaroff,Ellen
;  APPLICANT:  Gao,Wei-Qiang
;  APPLICANT:  Gerritsen,Mary E.
;  APPLICANT:  Goddard,Audrey
;  APPLICANT:  Godowski,Paul J.
;  APPLICANT:  Gurney,Austin L.
;  APPLICANT:  Sherwood,Steven
;  APPLICANT:  Smith,Victoria
;  APPLICANT:  Stewart,Timothy A.
;  APPLICANT:  Tumas,Daniel
;  APPLICANT:  Watanabe,Colin K
;  APPLICANT:  Wood,William
;  APPLICANT:  Zhang, Zemin
;  TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
;  TITLE OF INVENTION:  ACIDS ENCODING THE SAME
;  FILE REFERENCE: P3330R1C288
;  CURRENT APPLICATION NUMBER: US/10/176,921
;  CURRENT FILING DATE:  2002-06-20
;  Prior Application removed - See File Wrapper or Palm
;  NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 46
;   LENGTH: 586
;   TYPE: PRT
;   ORGANISM: Homo Sapien
US-10-176-921-46

  Query Match             92.5%;  Score 2815;  DB 14;  Length 586;
  Best Local Similarity   100.0%;  Pred. No. 9.9e-197;
  Matches  549;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MALEIHMSDPMCLIENFNEQLKVNQEALEILSAITQPVVVVAIVGLYRTGKSYLMNKLAG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MALEIHMSDPMCLIENFNEQLKVNQEALEILSAITQPVVVVAIVGLYRTGKSYLMNKLAG 60

Qy         61 KNKGFSVASTVQSHTKGIWIWCVPHPNWPNHTLVLLDTEGLGDVEKADNKNDIQIFALAL 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 KNKGFSVASTVQSHTKGIWIWCVPHPNWPNHTLVLLDTEGLGDVEKADNKNDIQIFALAL 120

Qy        121 LLSSTFVYNTVNKIDQGAIDLLHNVTELTDLLKARNSPDLDRVEDPADSASFFPDLVWTL 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 LLSSTFVYNTVNKIDQGAIDLLHNVTELTDLLKARNSPDLDRVEDPADSASFFPDLVWTL 180

Qy        181 RDFCLGLEIDGQLVTPDEYLENSLRPKQGSDQRVQNFNLPRLCIQKFFPKKKCFIFDLPA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 RDFCLGLEIDGQLVTPDEYLENSLRPKQGSDQRVQNFNLPRLCIQKFFPKKKCFIFDLPA 240

Qy        241 HQKKLAQLETLPDDELEPEFVQQVTEFCSYIFSHSMTKTLPGGIMVNGSRLKNLVLTYVN 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 HQKKLAQLETLPDDELEPEFVQQVTEFCSYIFSHSMTKTLPGGIMVNGSRLKNLVLTYVN 300

Qy        301 AISSGDLPCIENAVLALAQRENSAAVQKAIAHYDQQMGQKVQLPMETLQELLDLHRTSER 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 AISSGDLPCIENAVLALAQRENSAAVQKAIAHYDQQMGQKVQLPMETLQELLDLHRTSER 360

Qy        361 EAIEVFMKNSFKDVDQSFQKELETLLDAKQNDICKRNLEASSDYCSALLKDIFGPLEEAV 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 EAIEVFMKNSFKDVDQSFQKELETLLDAKQNDICKRNLEASSDYCSALLKDIFGPLEEAV 420

Qy        421 KQGIYSKPGGHNLFIQKTEELKAKYYREPRKGIQAEEVLQKYLKSKESVSHAILQTDQAL 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 KQGIYSKPGGHNLFIQKTEELKAKYYREPRKGIQAEEVLQKYLKSKESVSHAILQTDQAL 480

Qy        481 TETEKKKKEAQVKAEAEKAEAQRLAAIQRQNEQMMQERERLHQEQVRQMEIAKQNWLAEQ 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 TETEKKKKEAQVKAEAEKAEAQRLAAIQRQNEQMMQERERLHQEQVRQMEIAKQNWLAEQ 540

Qy        541 QKMQEQQMQ 549
              |||||||||
Db        541 QKMQEQQMQ 549


RESULT 10
US-10-137-865-46
; Sequence 46, Application US/10137865
; Publication No. US20030032155A1
; GENERAL INFORMATION:
;  APPLICANT: Baker,Kevin P.
;  APPLICANT:  Beresini,Maureen
;  APPLICANT:  DeForge,Laura
;  APPLICANT:  Desnoyers,Luc
;  APPLICANT:  Filvaroff,Ellen
;  APPLICANT:  Gao,Wei-Qiang
;  APPLICANT:  Gerritsen,Mary E.
;  APPLICANT:  Goddard,Audrey
;  APPLICANT:  Godowski,Paul J.
;  APPLICANT:  Gurney,Austin L.
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;  APPLICANT:  Sherwood,Steven
;  APPLICANT:  Smith,Victoria
;  APPLICANT:  Stewart,Timothy A.
;  APPLICANT:  Tumas,Daniel
;  APPLICANT:  Watanabe,Colin K
;  APPLICANT:  Wood,William
;  APPLICANT:  Zhang, Zemin
;  TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
;  TITLE OF INVENTION:  ACIDS ENCODING THE SAME
;  FILE REFERENCE: P3330R1C154
;  CURRENT APPLICATION NUMBER: US/10/137,865
;  CURRENT FILING DATE:  2002-05-03
;  Prior Application removed - See Palm or File Wrapper
;  NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 46
;   LENGTH: 586
;   TYPE: PRT
;   ORGANISM: Homo Sapien
US-10-137-865-46

  Query Match             92.5%;  Score 2815;  DB 14;  Length 586;
  Best Local Similarity   100.0%;  Pred. No. 9.9e-197;
  Matches  549;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MALEIHMSDPMCLIENFNEQLKVNQEALEILSAITQPVVVVAIVGLYRTGKSYLMNKLAG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MALEIHMSDPMCLIENFNEQLKVNQEALEILSAITQPVVVVAIVGLYRTGKSYLMNKLAG 60

Qy         61 KNKGFSVASTVQSHTKGIWIWCVPHPNWPNHTLVLLDTEGLGDVEKADNKNDIQIFALAL 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 KNKGFSVASTVQSHTKGIWIWCVPHPNWPNHTLVLLDTEGLGDVEKADNKNDIQIFALAL 120

Qy        121 LLSSTFVYNTVNKIDQGAIDLLHNVTELTDLLKARNSPDLDRVEDPADSASFFPDLVWTL 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 LLSSTFVYNTVNKIDQGAIDLLHNVTELTDLLKARNSPDLDRVEDPADSASFFPDLVWTL 180

Qy        181 RDFCLGLEIDGQLVTPDEYLENSLRPKQGSDQRVQNFNLPRLCIQKFFPKKKCFIFDLPA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 RDFCLGLEIDGQLVTPDEYLENSLRPKQGSDQRVQNFNLPRLCIQKFFPKKKCFIFDLPA 240

Qy        241 HQKKLAQLETLPDDELEPEFVQQVTEFCSYIFSHSMTKTLPGGIMVNGSRLKNLVLTYVN 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 HQKKLAQLETLPDDELEPEFVQQVTEFCSYIFSHSMTKTLPGGIMVNGSRLKNLVLTYVN 300

Qy        301 AISSGDLPCIENAVLALAQRENSAAVQKAIAHYDQQMGQKVQLPMETLQELLDLHRTSER 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 AISSGDLPCIENAVLALAQRENSAAVQKAIAHYDQQMGQKVQLPMETLQELLDLHRTSER 360

Qy        361 EAIEVFMKNSFKDVDQSFQKELETLLDAKQNDICKRNLEASSDYCSALLKDIFGPLEEAV 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 EAIEVFMKNSFKDVDQSFQKELETLLDAKQNDICKRNLEASSDYCSALLKDIFGPLEEAV 420

Qy        421 KQGIYSKPGGHNLFIQKTEELKAKYYREPRKGIQAEEVLQKYLKSKESVSHAILQTDQAL 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 KQGIYSKPGGHNLFIQKTEELKAKYYREPRKGIQAEEVLQKYLKSKESVSHAILQTDQAL 480

Qy        481 TETEKKKKEAQVKAEAEKAEAQRLAAIQRQNEQMMQERERLHQEQVRQMEIAKQNWLAEQ 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 TETEKKKKEAQVKAEAEKAEAQRLAAIQRQNEQMMQERERLHQEQVRQMEIAKQNWLAEQ 540

Qy        541 QKMQEQQMQ 549
              |||||||||
Db        541 QKMQEQQMQ 549


RESULT 11
US-10-140-474-46
; Sequence 46, Application US/10140474
; Publication No. US20030032156A1
; GENERAL INFORMATION:
;  APPLICANT: Baker,Kevin P.
;  APPLICANT:  Beresini,Maureen
;  APPLICANT:  DeForge,Laura
;  APPLICANT:  Desnoyers,Luc
;  APPLICANT:  Filvaroff,Ellen
;  APPLICANT:  Gao,Wei-Qiang
;  APPLICANT:  Gerritsen,Mary E.
;  APPLICANT:  Goddard,Audrey
;  APPLICANT:  Godowski,Paul J.
;  APPLICANT:  Gurney,Austin L.
;  APPLICANT:  Sherwood,Steven
;  APPLICANT:  Smith,Victoria
;  APPLICANT:  Stewart,Timothy A.
;  APPLICANT:  Tumas,Daniel
;  APPLICANT:  Watanabe,Colin K
;  APPLICANT:  Wood,William
;  APPLICANT:  Zhang, Zemin
;  TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
;  TITLE OF INVENTION:  ACIDS ENCODING THE SAME
;  FILE REFERENCE: P3330R1C162
;  CURRENT APPLICATION NUMBER: US/10/140,474
;  CURRENT FILING DATE:  2002-05-06
;  Prior Application removed - See Palm or File Wrapper
;  NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 46
;   LENGTH: 586
;   TYPE: PRT
;   ORGANISM: Homo Sapien
US-10-140-474-46

  Query Match             92.5%;  Score 2815;  DB 14;  Length 586;
  Best Local Similarity   100.0%;  Pred. No. 9.9e-197;
  Matches  549;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MALEIHMSDPMCLIENFNEQLKVNQEALEILSAITQPVVVVAIVGLYRTGKSYLMNKLAG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MALEIHMSDPMCLIENFNEQLKVNQEALEILSAITQPVVVVAIVGLYRTGKSYLMNKLAG 60

Qy         61 KNKGFSVASTVQSHTKGIWIWCVPHPNWPNHTLVLLDTEGLGDVEKADNKNDIQIFALAL 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 KNKGFSVASTVQSHTKGIWIWCVPHPNWPNHTLVLLDTEGLGDVEKADNKNDIQIFALAL 120

Qy        121 LLSSTFVYNTVNKIDQGAIDLLHNVTELTDLLKARNSPDLDRVEDPADSASFFPDLVWTL 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 LLSSTFVYNTVNKIDQGAIDLLHNVTELTDLLKARNSPDLDRVEDPADSASFFPDLVWTL 180

Qy        181 RDFCLGLEIDGQLVTPDEYLENSLRPKQGSDQRVQNFNLPRLCIQKFFPKKKCFIFDLPA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 RDFCLGLEIDGQLVTPDEYLENSLRPKQGSDQRVQNFNLPRLCIQKFFPKKKCFIFDLPA 240

Qy        241 HQKKLAQLETLPDDELEPEFVQQVTEFCSYIFSHSMTKTLPGGIMVNGSRLKNLVLTYVN 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 HQKKLAQLETLPDDELEPEFVQQVTEFCSYIFSHSMTKTLPGGIMVNGSRLKNLVLTYVN 300

Qy        301 AISSGDLPCIENAVLALAQRENSAAVQKAIAHYDQQMGQKVQLPMETLQELLDLHRTSER 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 AISSGDLPCIENAVLALAQRENSAAVQKAIAHYDQQMGQKVQLPMETLQELLDLHRTSER 360

Qy        361 EAIEVFMKNSFKDVDQSFQKELETLLDAKQNDICKRNLEASSDYCSALLKDIFGPLEEAV 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 EAIEVFMKNSFKDVDQSFQKELETLLDAKQNDICKRNLEASSDYCSALLKDIFGPLEEAV 420

Qy        421 KQGIYSKPGGHNLFIQKTEELKAKYYREPRKGIQAEEVLQKYLKSKESVSHAILQTDQAL 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 KQGIYSKPGGHNLFIQKTEELKAKYYREPRKGIQAEEVLQKYLKSKESVSHAILQTDQAL 480

Qy        481 TETEKKKKEAQVKAEAEKAEAQRLAAIQRQNEQMMQERERLHQEQVRQMEIAKQNWLAEQ 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 TETEKKKKEAQVKAEAEKAEAQRLAAIQRQNEQMMQERERLHQEQVRQMEIAKQNWLAEQ 540

Qy        541 QKMQEQQMQ 549
              |||||||||
Db        541 QKMQEQQMQ 549


RESULT 12
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US-10-142-431-46
; Sequence 46, Application US/10142431
; Publication No. US20030036179A1
; GENERAL INFORMATION:
; APPLICANT: Baker,Kevin P.
; APPLICANT: Beresini,Maureen
; APPLICANT: DeForge,Laura
; APPLICANT: Desnoyers,Luc
; APPLICANT: Filvaroff,Ellen
; APPLICANT: Gao,Wei-Qiang
; APPLICANT: Gerritsen,Mary E.
; APPLICANT: Goddard,Audrey
; APPLICANT: Godowski,Paul J.
; APPLICANT: Gurney,Austin L.
; APPLICANT: Sherwood,Steven
; APPLICANT: Smith,Victoria
; APPLICANT: Stewart,Timothy A.
; APPLICANT: Tumas,Daniel
; APPLICANT: Watanabe,Colin K
; APPLICANT: Wood,William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3330R1C251
; CURRENT APPLICATION NUMBER: US/10/142,431
; CURRENT FILING DATE: 2002-05-10
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 46
; LENGTH: 586
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-142-431-46

Query Match 92.5%; Score 2815; DB 14; Length 586;
Best Local Similarity 100.0%; Pred. No. 9.9e-197;
Matches 549; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 MALEIHMSDPMCLIENFNEQLKVNQEALEILSAITQPVVVVAIVGLYRTGKSYLMNKLAG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MALEIHMSDPMCLIENFNEQLKVNQEALEILSAITQPVVVVAIVGLYRTGKSYLMNKLAG 60

Qy         61 KNKGFSVASTVQSHTKGIWIWCVPHPNWPNHTLVLLDTEGLGDVEKADNKNDIQIFALAL 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 KNKGFSVASTVQSHTKGIWIWCVPHPNWPNHTLVLLDTEGLGDVEKADNKNDIQIFALAL 120

Qy        121 LLSSTFVYNTVNKIDQGAIDLLHNVTELTDLLKARNSPDLDRVEDPADSASFFPDLVWTL 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 LLSSTFVYNTVNKIDQGAIDLLHNVTELTDLLKARNSPDLDRVEDPADSASFFPDLVWTL 180

Qy        181 RDFCLGLEIDGQLVTPDEYLENSLRPKQGSDQRVQNFNLPRLCIQKFFPKKKCFIFDLPA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 RDFCLGLEIDGQLVTPDEYLENSLRPKQGSDQRVQNFNLPRLCIQKFFPKKKCFIFDLPA 240

Qy        241 HQKKLAQLETLPDDELEPEFVQQVTEFCSYIFSHSMTKTLPGGIMVNGSRLKNLVLTYVN 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 HQKKLAQLETLPDDELEPEFVQQVTEFCSYIFSHSMTKTLPGGIMVNGSRLKNLVLTYVN 300

Qy        301 AISSGDLPCIENAVLALAQRENSAAVQKAIAHYDQQMGQKVQLPMETLQELLDLHRTSER 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 AISSGDLPCIENAVLALAQRENSAAVQKAIAHYDQQMGQKVQLPMETLQELLDLHRTSER 360

Qy        361 EAIEVFMKNSFKDVDQSFQKELETLLDAKQNDICKRNLEASSDYCSALLKDIFGPLEEAV 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 EAIEVFMKNSFKDVDQSFQKELETLLDAKQNDICKRNLEASSDYCSALLKDIFGPLEEAV 420

Qy        421 KQGIYSKPGGHNLFIQKTEELKAKYYREPRKGIQAEEVLQKYLKSKESVSHAILQTDQAL 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 KQGIYSKPGGHNLFIQKTEELKAKYYREPRKGIQAEEVLQKYLKSKESVSHAILQTDQAL 480

Qy        481 TETEKKKKEAQVKAEAEKAEAQRLAAIQRQNEQMMQERERLHQEQVRQMEIAKQNWLAEQ 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 TETEKKKKEAQVKAEAEKAEAQRLAAIQRQNEQMMQERERLHQEQVRQMEIAKQNWLAEQ 540

Qy        541 QKMQEQQMQ 549
              |||||||||
Db        541 QKMQEQQMQ 549
```

RESULT 13
US-10-143-114-46
; Sequence 46, Application US/10143114
; Publication No. US20030036180A1
; GENERAL INFORMATION:
; APPLICANT: Baker,Kevin P.
; APPLICANT: Beresini,Maureen
; APPLICANT: DeForge,Laura
; APPLICANT: Desnoyers,Luc
; APPLICANT: Filvaroff,Ellen
; APPLICANT: Gao,Wei-Qiang
; APPLICANT: Gerritsen,Mary E.
; APPLICANT: Goddard,Audrey
; APPLICANT: Godowski,Paul J.
; APPLICANT: Gurney,Austin L.
; APPLICANT: Sherwood,Steven
; APPLICANT: Smith,Victoria
; APPLICANT: Stewart,Timothy A.
; APPLICANT: Tumas,Daniel
; APPLICANT: Watanabe,Colin K
; APPLICANT: Wood,William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3330R1C211
; CURRENT APPLICATION NUMBER: US/10/143,114
; CURRENT FILING DATE: 2002-05-09
; Prior Application removed - See Palm or File Wrapper
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 46
; LENGTH: 586
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-143-114-46

Query Match 92.5%; Score 2815; DB 14; Length 586;
Best Local Similarity 100.0%; Pred. No. 9.9e-197;
Matches 549; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 MALEIHMSDPMCLIENFNEQLKVNQEALEILSAITQPVVVVAIVGLYRTGKSYLMNKLAG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MALEIHMSDPMCLIENFNEQLKVNQEALEILSAITQPVVVVAIVGLYRTGKSYLMNKLAG 60

Qy         61 KNKGFSVASTVQSHTKGIWIWCVPHPNWPNHTLVLLDTEGLGDVEKADNKNDIQIFALAL 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 KNKGFSVASTVQSHTKGIWIWCVPHPNWPNHTLVLLDTEGLGDVEKADNKNDIQIFALAL 120

Qy        121 LLSSTFVYNTVNKIDQGAIDLLHNVTELTDLLKARNSPDLDRVEDPADSASFFPDLVWTL 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 LLSSTFVYNTVNKIDQGAIDLLHNVTELTDLLKARNSPDLDRVEDPADSASFFPDLVWTL 180

Qy        181 RDFCLGLEIDGQLVTPDEYLENSLRPKQGSDQRVQNFNLPRLCIQKFFPKKKCFIFDLPA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 RDFCLGLEIDGQLVTPDEYLENSLRPKQGSDQRVQNFNLPRLCIQKFFPKKKCFIFDLPA 240

Qy        241 HQKKLAQLETLPDDELEPEFVQQVTEFCSYIFSHSMTKTLPGGIMVNGSRLKNLVLTYVN 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 HQKKLAQLETLPDDELEPEFVQQVTEFCSYIFSHSMTKTLPGGIMVNGSRLKNLVLTYVN 300

Qy        301 AISSGDLPCIENAVLALAQRENSAAVQKAIAHYDQQMGQKVQLPMETLQELLDLHRTSER 360
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Db        301 AISSGDLPCIENAVLALAQRENSAAVQKAIAHYDQQMGQKVQLPMETLQELLDLHRTSER 360

Qy        361 EAIEVFMKNSFKDVDQSFQKELETLLDAKQNDICKRNLEASSDYCSALLKDIFGPLEEAV 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 EAIEVFMKNSFKDVDQSFQKELETLLDAKQNDICKRNLEASSDYCSALLKDIFGPLEEAV 420
```

```
Qy        421 KQGIYSKPGGHNLFIQKTEELKAKYYREPRKGIQAEEVLQKYLKSKESVSHAILQTDQAL 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 KQGIYSKPGGHNLFIQKTEELKAKYYREPRKGIQAEEVLQKYLKSKESVSHAILQTDQAL 480

Qy        481 TETEKKKKEAQVKAEAEKAEAQRLAAIQRQNEQMMQERERLHQEQVRQMEIAKQNWLAEQ 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 TETEKKKKEAQVKAEAEKAEAQRLAAIQRQNEQMMQERERLHQEQVRQMEIAKQNWLAEQ 540

Qy        541 QKMQEQQMQ 549
              |||||||||
Db        541 QKMQEQQMQ 549


RESULT 14
US-10-142-419-46
; Sequence 46, Application US/10142419
; Publication No. US20030044945A1
; GENERAL INFORMATION:
;  APPLICANT: Baker,Kevin P.
;  APPLICANT:  Beresini,Maureen
;  APPLICANT:  DeForge,Laura
;  APPLICANT:  Desnoyers,Luc
;  APPLICANT:  Filvaroff,Ellen
;  APPLICANT:  Gao,Wei-Qiang
;  APPLICANT:  Gerritsen,Mary E.
;  APPLICANT:  Goddard,Audrey
;  APPLICANT:  Godowski,Paul J.
;  APPLICANT:  Gurney,Austin L.
;  APPLICANT:  Sherwood,Steven
;  APPLICANT:  Smith,Victoria
;  APPLICANT:  Stewart,Timothy A.
;  APPLICANT:  Tumas,Daniel
;  APPLICANT:  Watanabe,Colin K
;  APPLICANT:  Wood,William
;  APPLICANT:  Zhang, Zemin
;  TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
;  TITLE OF INVENTION:  ACIDS ENCODING THE SAME
;  FILE REFERENCE: P3330R1C244
;  CURRENT APPLICATION NUMBER: US/10/142,419
;  CURRENT FILING DATE:  2002-05-10
;  Prior Apploication removed - See File Wrapper or Palm
;  NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 46
;   LENGTH: 586
;   TYPE: PRT
;   ORGANISM: Homo Sapien
US-10-142-419-46

  Query Match             92.5%;  Score 2815;  DB 14;  Length 586;
  Best Local Similarity   100.0%;  Pred. No. 9.9e-197;
  Matches  549;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MALEIHMSDPMCLIENFNEQLKVNQEALEILSAITQPVVVVAIVGLYRTGKSYLMNKLAG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MALEIHMSDPMCLIENFNEQLKVNQEALEILSAITQPVVVVAIVGLYRTGKSYLMNKLAG 60

Qy         61 KNKGFSVASTVQSHTKGIWIWCVPHPNWPNHTLVLLDTEGLGDVEKADNKNDIQIFALAL 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 KNKGFSVASTVQSHTKGIWIWCVPHPNWPNHTLVLLDTEGLGDVEKADNKNDIQIFALAL 120

Qy        121 LLSSTFVYNTVNKIDQGAIDLLHNVTELTDLLKARNSPDLDRVEDPADSASFFPDLVWTL 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 LLSSTFVYNTVNKIDQGAIDLLHNVTELTDLLKARNSPDLDRVEDPADSASFFPDLVWTL 180

Qy        181 RDFCLGLEIDGQLVTPDEYLENSLRPKQGSDQRVQNFNLPRLCIQKFFPKKKCFIFDLPA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 RDFCLGLEIDGQLVTPDEYLENSLRPKQGSDQRVQNFNLPRLCIQKFFPKKKCFIFDLPA 240

Qy        241 HQKKLAQLETLPDDELEPEFVQQVTEFCSYIFSHSMTKTLPGGIMVNGSRLKNLVLTYVN 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 HQKKLAQLETLPDDELEPEFVQQVTEFCSYIFSHSMTKTLPGGIMVNGSRLKNLVLTYVN 300

Qy        301 AISSGDLPCIENAVLALAQRENSAAVQKAIAHYDQQMGQKVQLPMETLQELLDLHRTSER 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 AISSGDLPCIENAVLALAQRENSAAVQKAIAHYDQQMGQKVQLPMETLQELLDLHRTSER 360

Qy        361 EAIEVFMKNSFKDVDQSFQKELETLLDAKQNDICKRNLEASSDYCSALLKDIFGPLEEAV 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 EAIEVFMKNSFKDVDQSFQKELETLLDAKQNDICKRNLEASSDYCSALLKDIFGPLEEAV 420

Qy        421 KQGIYSKPGGHNLFIQKTEELKAKYYREPRKGIQAEEVLQKYLKSKESVSHAILQTDQAL 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 KQGIYSKPGGHNLFIQKTEELKAKYYREPRKGIQAEEVLQKYLKSKESVSHAILQTDQAL 480

Qy        481 TETEKKKKEAQVKAEAEKAEAQRLAAIQRQNEQMMQERERLHQEQVRQMEIAKQNWLAEQ 540
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Db        481 TETEKKKKEAQVKAEAEKAEAQRLAAIQRQNEQMMQERERLHQEQVRQMEIAKQNWLAEQ 540

Qy        541 QKMQEQQMQ 549
              |||||||||
Db        541 QKMQEQQMQ 549


RESULT 15
US-10-123-262-46
; Sequence 46, Application US/10123262
; Publication No. US20030049816A1
; GENERAL INFORMATION:
;  APPLICANT: Baker,Kevin P.
;  APPLICANT:  Beresini,Maureen
;  APPLICANT:  DeForge,Laura
;  APPLICANT:  Desnoyers,Luc
;  APPLICANT:  Filvaroff,Ellen
;  APPLICANT:  Gao,Wei-Qiang
;  APPLICANT:  Gerritsen,Mary E.
;  APPLICANT:  Goddard,Audrey
;  APPLICANT:  Godowski,Paul J.
;  APPLICANT:  Gurney,Austin L.
;  APPLICANT:  Sherwood,Steven
;  APPLICANT:  Smith,Victoria
;  APPLICANT:  Stewart,Timothy A.
;  APPLICANT:  Tumas,Daniel
;  APPLICANT:  Watanabe,Colin K
;  APPLICANT:  Wood,William
;  APPLICANT:  Zhang, Zemin
;  TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
;  TITLE OF INVENTION:  ACIDS ENCODING THE SAME
;  FILE REFERENCE: P3330R1C38
;  CURRENT APPLICATION NUMBER: US/10/123,262
;  CURRENT FILING DATE:  2002-04-15
;  Prior Application removed - See File Wrapper or Palm
;  NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 46
;   LENGTH: 586
;   TYPE: PRT
;   ORGANISM: Homo Sapien
US-10-123-262-46

  Query Match             92.5%;  Score 2815;  DB 14;  Length 586;
  Best Local Similarity   100.0%;  Pred. No. 9.9e-197;
  Matches  549;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MALEIHMSDPMCLIENFNEQLKVNQEALEILSAITQPVVVVAIVGLYRTGKSYLMNKLAG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MALEIHMSDPMCLIENFNEQLKVNQEALEILSAITQPVVVVAIVGLYRTGKSYLMNKLAG 60

Qy         61 KNKGFSVASTVQSHTKGIWIWCVPHPNWPNHTLVLLDTEGLGDVEKADNKNDIQIFALAL 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy        121 LLSSTFVYNTVNKIDQGAIDLLHNVTELTDLLKARNSPDLDRVEDPADSASFFPDLVWTL 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 LLSSTFVYNTVNKIDQGAIDLLHNVTELTDLLKARNSPDLDRVEDPADSASFFPDLVWTL 180

Qy        181 RDFCLGLEIDGQLVTPDEYLENSLRPKQGSDQRVQNFNLPRLCIQKFFPKKKCFIFDLPA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db        181 RDFCLGLEIDGQLVTPDEYLENSLRPKQGSDQRVQNFNLPRLCIQKFFPKKKCFIFDLPA 240

Qy        241 HQKKLAQLETLPDDELEPEFVQQVTEFCSYIFSHSMTKTLPGGIMVNGSRLKNLVLTYVN 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 HQKKLAQLETLPDDELEPEFVQQVTEFCSYIFSHSMTKTLPGGIMVNGSRLKNLVLTYVN 300

Qy        301 AISSGDLPCIENAVLALAQRENSAAVQKAIAHYDQQMGQKVQLPMETLQELLDLHRTSER 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 AISSGDLPCIENAVLALAQRENSAAVQKAIAHYDQQMGQKVQLPMETLQELLDLHRTSER 360

Qy        361 EAIEVFMKNSFKDVDQSFQKELETLLDAKQNDICKRNLEASSDYCSALLKDIFGPLEEAV 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 EAIEVFMKNSFKDVDQSFQKELETLLDAKQNDICKRNLEASSDYCSALLKDIFGPLEEAV 420

Qy        421 KQGIYSKPGGHNLFIQKTEELKAKYYREPRKGIQAEEVLQKYLKSKESVSHAILQTDQAL 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 KQGIYSKPGGHNLFIQKTEELKAKYYREPRKGIQAEEVLQKYLKSKESVSHAILQTDQAL 480

Qy        481 TETEKKKKEAQVKAEAEKAEAQRLAAIQRQNEQMMQERERLHQEQVRQMEIAKQNWLAEQ 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 TETEKKKKEAQVKAEAEKAEAQRLAAIQRQNEQMMQERERLHQEQVRQMEIAKQNWLAEQ 540

Qy        541 QKMQEQQMQ 549
              |||||||||
Db        541 QKMQEQQMQ 549
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Search completed: July 9, 2005, 13:41:36
Job time : 164 secs

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: July 9, 2005, 13:15:14 ; Search time 168 Seconds
(without alignments)
1360.568 Million cell updates/sec

Title: US-10-659-549-3
Perfect score: 3043
Sequence: 1 MALEIHMSDPMCLIENFNEQ.....GEAARSCGSQQGVWSQKVWV 591

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Dec04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	3043	100.0	591	7	ADD95076	Add95076 Human gua
2	2815	92.5	586	4	AAU12194	Aau12194 Human PRO
3	2815	92.5	586	5	ABB77445	Abb77445 Human tum
4	2815	92.5	586	6	ABO17638	Abo17638 Novel hum
5	2815	92.5	586	6	ABU80892	Abu80892 Human PRO
6	2815	92.5	586	6	ABU66592	Abu66592 Human PRO
7	2815	92.5	586	6	ABU59673	Abu59673 Novel sec
8	2815	92.5	586	6	ABO24863	Abo24863 Human sec
9	2815	92.5	586	6	ABU66868	Abu66868 Human sec
10	2815	92.5	586	6	ADA45565	Ada45565 Novel hum
11	2815	92.5	586	6	ADA75996	Ada75996 Human PRO
12	2815	92.5	586	6	ADA18646	Ada18646 Human PRO
13	2815	92.5	586	6	ADA61269	Ada61269 Homo sapi
14	2815	92.5	586	6	ADB19054	Adb19054 Novel hum
15	2815	92.5	586	6	ADB27595	Adb27595 Human PRO
16	2815	92.5	586	6	ADA86074	Ada86074 Novel hum
17	2815	92.5	586	6	ADB15638	Adb15638 Human PRO
18	2815	92.5	586	6	ADA47424	Ada47424 Human PRO
19	2815	92.5	586	6	ADA67219	Ada67219 Human PRO
20	2815	92.5	586	6	ADB30226	Adb30226 Human PRO
21	2815	92.5	586	6	ADA85522	Ada85522 Novel hum
22	2815	92.5	586	6	ADA96734	Ada96734 Human PRO
23	2815	92.5	586	6	ADA79038	Ada79038 Human PRO
24	2815	92.5	586	6	ADA87177	Ada87177 Novel hum
25	2815	92.5	586	6	ADB16379	Adb16379 Human PRO
26	2815	92.5	586	6	ADA91471	Ada91471 Novel hum
27	2815	92.5	586	6	ADB14534	Adb14534 Human PRO
28	2815	92.5	586	6	ADB18495	Adb18495 Novel hum
29	2815	92.5	586	6	ADA93710	Ada93710 Human PRO
30	2815	92.5	586	6	ADB19606	Adb19606 Novel hum
31	2815	92.5	586	6	ADB12918	Adb12918 Human PRO
32	2815	92.5	586	6	ABO43171	Abo43171 Novel hum
33	2815	92.5	586	6	ADA74172	Ada74172 Human PRO
34	2815	92.5	586	6	ADB24405	Adb24405 Human PRO
35	2815	92.5	586	6	ADA81929	Ada81929 Human PRO
36	2815	92.5	586	6	ADA74892	Ada74892 Human PRO
37	2815	92.5	586	6	ADA84970	Ada84970 Novel hum
38	2815	92.5	586	6	ADA84418	Ada84418 Novel hum
39	2815	92.5	586	6	ADB29674	Adb29674 Human PRO
40	2815	92.5	586	6	ADA80202	Ada80202 Human PRO
41	2815	92.5	586	6	ADA75444	Ada75444 Human PRO
42	2815	92.5	586	6	ADA46669	Ada46669 Human PRO
43	2815	92.5	586	6	ADB24965	Adb24965 Human PRO
44	2815	92.5	586	6	ADA93141	Ada93141 Human PRO
45	2815	92.5	586	6	ADB26491	Adb26491 Human PRO

ALIGNMENTS

RESULT 1
ADD95076
ID ADD95076 standard; protein; 591 AA.
XX
AC ADD95076;
XX
DT 29-JAN-2004 (first entry)
XX
DE Human guanylate binding protein-4 (GBP-4).
XX
KW Human; guanylate binding protein-4; GBP-4; myelodysplastic disorder;
KW myeloproliferative syndrome; acute myeloid leukaemia; cancer; gastric;
KW lung; colon; melanoma; multiple sclerosis; lung disorder;
KW intestinal-related disorder; interferon-gamma-induced response;
KW macrophage; fibroblast; immune cell; neuroprotective; cytostatic.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Binding-site 97. .100
FT /label= GTP-binding_consensus_motif
FT /note= "Specifically claimed in Claim 26"
FT Modified-site 179. .182
FT /label= Potential_casein_kinase_II_phosphorylation_site
FT /note= "Specifically claimed in Claim 26"
FT Modified-site 179. .181
FT /label= Potential_protein_kinase_C_phosphorylation_site
FT /note= "Specifically claimed in Claim 26"
FT Modified-site 283. .288
FT /label= Potential_N-myristoylation_site
FT /note= "Specifically claimed in Claim 26"
FT Modified-site 554. .557
FT /label= Potential_prenylation_site
FT /note= "Specifically claimed in Claim 26"
FT Modified-site 562. .564
FT /label= Potential_protein_kinase_C_phosphorylation_site
FT /note= "Specifically claimed in Claim 26"
FT Modified-site 568. .571
FT /label= Potential_casein_kinase_II_phosphorylation_site
FT /note= "Specifically claimed in Claim 26"
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FT /label= Potential_N-myristoylation_site
FT /note= "Specifically claimed in Claim 26"
FT Modified-site 586. .588
FT /label= Potential_protein_kinase_C_phosphorylation_site

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FT                   /note= "Specifically claimed in Claim 26"
XX
PN   US6642024-B1.
XX
PD   04-NOV-2003.
XX
PF   17-AUG-2000; 2000US-00643657.
XX
PR   29-JAN-1998;   98US-00015089.
XX
PA   (GETH ) GENENTECH INC.
XX
PI   Pennica D;
XX
DR   WPI; 2003-851360/79.
DR   N-PSDB; ADD95074, ADD95105.
XX
PT   New isolated nucleic encoding guanylate binding protein-4, useful as
PT   hybridization probes, in chromosome and gene mapping, treating cancer,
PT   e.g. gastric cancer or melanoma or combating immunological and
PT   inflammatory responses.
XX
PS   Claim 1; SEQ ID NO 3; 60pp; English.
XX
CC   The present invention relates to the isolation of a novel human guanylate
CC   binding protein (guanylate binding protein-4 or GBP-4), and the
CC   polynucleotide sequence encoding it. The polynucleotide sequence encoding
CC   GBP-4, the GBP-4 polypeptide, and antibodies to GBP-4 are useful in
CC   treating myelodysplastic disorders, myeloproliferative syndromes, acute
CC   myeloid leukaemia and cancers (e.g. gastric, lung or colon cancers or
CC   melanoma). The polynucleotide sequence is useful as hybridisation probes,
CC   in chromosome and gene mapping, in generating transgenic animals, in
CC   radioimmunoassays, in inducing formation of anti-GBP-4 antibodies, in
CC   combating immunological and inflammatory responses and other pathological
CC   conditions (e.g. multiple sclerosis or lung and intestinal-related
CC   disorders), as a mediator of any interferon-gamma-induced responses in
CC   macrophages and fibroblasts, and may also function in other immune cell
CC   populations or in protein processing. The present sequence represents
CC   human GBP-4.
XX
SQ   Sequence 591 AA;

  Query Match            100.0%;  Score 3043;  DB 7;  Length 591;
  Best Local Similarity  100.0%;  Pred. No. 2.1e-241;
  Matches  591;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MALEIHMSDPMCLIENFNEQLKVNQEALEILSAITQPVVVVAIVGLYRTGKSYLMNKLAG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MALEIHMSDPMCLIENFNEQLKVNQEALEILSAITQPVVVVAIVGLYRTGKSYLMNKLAG 60

Qy         61 KNKGFSVASTVQSHTKGIWIWCVPHPNWPNHTLVLLDTEGLGDVEKADNKNDIQIFALAL 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 KNKGFSVASTVQSHTKGIWIWCVPHPNWPNHTLVLLDTEGLGDVEKADNKNDIQIFALAL 120

Qy        121 LLSSTFVYNTVNKIDQGAIDLLHNVTELTDLLKARNSPDLDRVEDPADSASFFPDLVWTL 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 LLSSTFVYNTVNKIDQGAIDLLHNVTELTDLLKARNSPDLDRVEDPADSASFFPDLVWTL 180

Qy        181 RDFCLGLEIDGQLVTPDEYLENSLRPKQGSDQRVQNFNLPRLCIQKFFPKKKCFIFDLPA 240
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Db        181 RDFCLGLEIDGQLVTPDEYLENSLRPKQGSDQRVQNFNLPRLCIQKFFPKKKCFIFDLPA 240

Qy        241 HQKKLAQLETLPDDELEPEFVQQVTEFCSYIFSHSMTKTLPGGIMVNGSRLKNLVLTYVN 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 HQKKLAQLETLPDDELEPEFVQQVTEFCSYIFSHSMTKTLPGGIMVNGSRLKNLVLTYVN 300

Qy        301 AISSGDLPCIENAVLALAQRENSAAVQKAIAHYDQQMGQKVQLPMETLQELLDLHRTSER 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 AISSGDLPCIENAVLALAQRENSAAVQKAIAHYDQQMGQKVQLPMETLQELLDLHRTSER 360

Qy        361 EAIEVFMKNSFKDVDQSFQKELETLLDAKQNDICKRNLEASSDYCSALLKDIFGPLEEAV 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 EAIEVFMKNSFKDVDQSFQKELETLLDAKQNDICKRNLEASSDYCSALLKDIFGPLEEAV 420

Qy        421 KQGIYSKPGGHNLFIQKTEELKAKYYREPRKGIQAEEVLQKYLKSKESVSHAILQTDQAL 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 KQGIYSKPGGHNLFIQKTEELKAKYYREPRKGIQAEEVLQKYLKSKESVSHAILQTDQAL 480

Qy        481 TETEKKKKEAQVKAEAEKAEAQRLAAIQRQNEQMMQERERLHQEQVRQMEIAKQNWLAEQ 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 TETEKKKKEAQVKAEAEKAEAQRLAAIQRQNEQMMQERERLHQEQVRQMEIAKQNWLAEQ 540

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              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 QKMQEQQMQVFINCFISPLPVTMRVCSSGKEGEAARSCGSQQGVWSQKVWV 591


RESULT 2
AAU12194
ID   AAU12194 standard; protein; 586 AA.
XX
AC   AAU12194;
XX
DT   24-OCT-2001  (first entry)
XX
DE   Human PRO4987 polypeptide sequence.
XX
KW   Human secretory and transmembrane; PRO; mammalian; cancer; lung; breast;
KW   prostate; cervical; tumour necrosis factor-alpha; TNF-alpha; cartilage;
KW   ear; proliferation; glucose; free fatty acid; skeletal muscle; adipocyte;
KW   A-peptide; factor VIIA; gene therapy.
XX
OS   Homo sapiens.
XX
PN   WO200140466-A2.
XX
PD   07-JUN-2001.
XX
PF   01-DEC-2000; 2000WO-US032678.
XX
PR   01-DEC-1999;   99WO-US028301.
PR   01-DEC-1999;   99WO-US028634.
PR   02-DEC-1999;   99WO-US028551.
PR   02-DEC-1999;   99WO-US028564.
PR   02-DEC-1999;   99WO-US028565.
PR   09-DEC-1999;   99US-0170262P.
PR   16-DEC-1999;   99WO-US030095.
PR   20-DEC-1999;   99WO-US030911.
PR   20-DEC-1999;   99WO-US030999.
PR   30-DEC-1999;   99WO-US031243.
PR   30-DEC-1999;   99WO-US031274.
PR   05-JAN-2000; 2000WO-US000219.
PR   06-JAN-2000; 2000WO-US000277.
PR   06-JAN-2000; 2000WO-US000376.
PR   11-FEB-2000; 2000WO-US003565.
PR   18-FEB-2000; 2000WO-US004341.
PR   18-FEB-2000; 2000WO-US004342.
PR   22-FEB-2000; 2000WO-US004414.
PR   24-FEB-2000; 2000WO-US004914.
PR   24-FEB-2000; 2000WO-US005004.
PR   01-MAR-2000; 2000WO-US005601.
PR   02-MAR-2000; 2000WO-US005841.
PR   03-MAR-2000; 2000US-0187202P.
PR   10-MAR-2000; 2000WO-US006319.
PR   15-MAR-2000; 2000WO-US006884.
PR   20-MAR-2000; 2000WO-US007377.
PR   21-MAR-2000; 2000WO-US007532.
PR   30-MAR-2000; 2000WO-US008439.
PR   17-MAY-2000; 2000WO-US013705.
PR   22-MAY-2000; 2000WO-US014042.
PR   30-MAY-2000; 2000WO-US014941.
PR   02-JUN-2000; 2000WO-US015264.
PR   05-JUN-2000; 2000US-0209832P.
PR   28-JUL-2000; 2000WO-US020710.
PR   11-AUG-2000; 2000WO-US022031.
PR   23-AUG-2000; 2000WO-US023522.
```

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: July 9, 2005, 13:18:54 ; Search time 172 Seconds
(without alignments)
1759.528 Million cell updates/sec

Title: US-10-659-549-3
Perfect score: 3043
Sequence: 1 MALEIHMSDPMCLIENFNEQ.....GEAARSCGSQQGVWSQKVWV 591

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_03:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	2815	92.5	586	1	GBP5_HUMAN	Q96pp8 homo sapien
2	2516	82.7	489	2	Q86TM5	Q86tm5 homo sapien
3	2490	81.8	504	2	Q8NF03	Q8nf03 homo sapien
4	2236	73.5	481	2	Q8N4Q4	Q8n4q4 homo sapien
5	1958.5	64.4	592	1	GBP1_HUMAN	P32455 homo sapien
6	1933	63.5	724	2	Q8BMN7	Q8bmn7 mus musculu
7	1907.5	62.7	590	1	GBP5_MOUSE	Q8cfb4 mus musculu
8	1905.5	62.6	561	2	Q8BU78	Q8bu78 mus musculu
9	1897	62.3	591	1	GBP2_HUMAN	P32456 homo sapien
10	1892	62.2	591	2	Q6GPH0	Q6gph0 homo sapien
11	1774.5	58.3	563	2	Q9H0R5	Q9h0r5 homo sapien
12	1765.5	58.0	589	1	GBP1_MOUSE	Q01514 mus musculu
13	1764	58.0	481	2	Q8TCE5	Q8tce5 homo sapien
14	1757.5	57.8	589	1	GBP2_RAT	Q63663 rattus norv
15	1750.5	57.5	589	1	GBP2_MOUSE	Q9z0e6 mus musculu
16	1528.5	50.2	638	2	Q8N8V2	Q8n8v2 homo sapien
17	1510.5	49.6	633	2	Q6ZN66	Q6zn66 homo sapien
18	1500.5	49.3	640	1	GBP4_HUMAN	Q96pp9 homo sapien
19	1498.5	49.2	640	2	Q6NSL0	Q6nsl0 homo sapien
20	1493.5	49.1	633	2	Q7Z3F0	Q7z3f0 homo sapien
21	1482.5	48.7	638	2	Q8BU48	Q8bu48 mus musculu
22	1482.5	48.7	641	2	Q6KAN1	Q6kan1 mus musculu
23	1479.5	48.6	632	2	Q91Z40	Q91z40 mus musculu
24	1468.5	48.3	620	2	Q8VEC5	Q8vec5 mus musculu
25	1459.5	48.0	620	2	Q61107	Q61107 mus musculu
26	1407	46.2	612	2	Q8CFA8	Q8cfa8 mus musculu
27	1392.5	45.8	611	2	Q6ZQL8	Q6zql8 mus musculu
28	1388.5	45.6	447	2	Q9NV33	Q9nv33 homo sapien
29	1377.5	45.3	611	2	Q6PEN2	Q6pen2 mus musculu
30	1365.5	44.9	623	2	Q61594	Q61594 mus musculu
31	1344	44.2	619	2	Q6PG83	Q6pg83 mus musculu
32	1342.5	44.1	595	2	Q6GN80	Q6gn80 xenopus lae
33	1335	43.9	619	2	Q8BTS3	Q8bts3 mus musculu
34	1333	43.8	587	2	Q6DCG7	Q6dcg7 xenopus lae
35	1325.5	43.6	607	2	Q7T0S6	Q7t0s6 xenopus lae
36	1259	41.4	620	2	Q66J21	Q66j21 xenopus lae
37	1229.5	40.4	528	2	Q66IR9	Q66ir9 xenopus lae
38	1198	39.4	635	2	Q6YLY1	Q6yly1 oncorhynchu
39	1183	38.9	621	2	Q6DHP7	Q6dhp7 brachydanio
40	1148.5	37.7	385	2	Q8K0G1	Q8k0g1 mus musculu
41	1097	36.0	290	2	Q6P3V3	Q6p3v3 homo sapien
42	1054	34.6	576	2	Q90892	Q90892 gallus gall
43	886	29.1	744	2	Q6PCI2	Q6pci2 xenopus lae
44	614.5	20.2	380	2	Q7TMV8	Q7tmv8 mus musculu
45	587.5	19.3	374	2	Q66K09	Q66k09 mus musculu

ALIGNMENTS

RESULT 1
GBP5_HUMAN
ID GBP5_HUMAN STANDARD; PRT; 586 AA.
AC Q96PP8;
DT 29-MAR-2004 (Rel. 43, Created)
DT 29-MAR-2004 (Rel. 43, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Interferon-induced guanylate-binding protein 5 (GTP-binding protein 5)
DE (Guanine nucleotide-binding protein 5) (GBP-TA antigen)
DE (UNQ2427/PRO4987).
GN Name=GBP5;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Avdalovic A., Fu H., Tsurushita N.;
RT "Human GBP-4 and -5: new members of the IFN-gamma-inducible guanylate
RT binding protein family.";
RL Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Eichmueller S., Hartmann T., Thiel D., Usener D., Dummer R.,
RA Schadendorf D.;
RT "GBP-TA: a new tumor-specific antigen of cutaneous lymphoma depicted
RT by serological detection.";
RL Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=22887296; PubMed=12975309; DOI=10.1101/gr.1293003;
RA Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Brush J.,
RA Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,
RA Eaton D., Foster J., Grimaldi C., Gu Q., Hass P.E., Heldens S.,
RA Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,
RA Lewis L., Liao D., Mark M., Robbie E., Sanchez C., Schoenfeld J.,
RA Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A.,
RA Vandlen R., Watanabe C., Wieand D., Woods K., Xie M.-H., Yansura D.,
RA Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I.,
RA Godowski P., Gray A.;
RT "The secreted protein discovery initiative (SPDI), a large-scale
RT effort to identify novel human secreted and transmembrane proteins: a
RT bioinformatics assessment.";
RL Genome Res. 13:2265-2270(2003).
RN [4]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

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RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC   -!- SIMILARITY: Belongs to the GBP family.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC   ---------------------------------------------------------------------
DR   EMBL; AF288815; AAL02055.1; -.
DR   EMBL; AF430642; AAN39035.1; -.
DR   EMBL; AF430643; AAN39036.1; -.
DR   EMBL; AY358953; AAQ89312.1; -.
DR   EMBL; BC031639; AAH31639.1; -.
DR   HSSP; P32455; 1DG3.
DR   Genew; HGNC:19895; GBP5.
DR   InterPro; IPR003191; GBP.
DR   Pfam; PF02263; GBP; 1.
DR   Pfam; PF02841; GBP_C; 1.
KW   GTP-binding; Lipoprotein; Multigene family; Prenylation.
FT   NP_BIND      45     52       GTP (By similarity).
FT   NP_BIND      97    101       GTP (By similarity).
FT   LIPID       583    583       S-geranylgeranyl cysteine (By
FT                                similarity).
SQ   SEQUENCE   586 AA;  66617 MW;  95DDC02F0FB705D0 CRC64;

  Query Match             92.5%;  Score 2815;  DB 1;  Length 586;
  Best Local Similarity   100.0%;  Pred. No. 1.7e-134;
  Matches  549;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MALEIHMSDPMCLIENFNEQLKVNQEALEILSAITQPVVVVAIVGLYRTGKSYLMNKLAG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MALEIHMSDPMCLIENFNEQLKVNQEALEILSAITQPVVVVAIVGLYRTGKSYLMNKLAG 60

Qy         61 KNKGFSVASTVQSHTKGIWIWCVPHPNWPNHTLVLLDTEGLGDVEKADNKNDIQIFALAL 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 KNKGFSVASTVQSHTKGIWIWCVPHPNWPNHTLVLLDTEGLGDVEKADNKNDIQIFALAL 120

Qy        121 LLSSTFVYNTVNKIDQGAIDLLHNVTELTDLLKARNSPDLDRVEDPADSASFFPDLVWTL 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 LLSSTFVYNTVNKIDQGAIDLLHNVTELTDLLKARNSPDLDRVEDPADSASFFPDLVWTL 180

Qy        181 RDFCLGLEIDGQLVTPDEYLENSLRPKQGSDQRVQNFNLPRLCIQKFFPKKKCFIFDLPA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 RDFCLGLEIDGQLVTPDEYLENSLRPKQGSDQRVQNFNLPRLCIQKFFPKKKCFIFDLPA 240

Qy        241 HQKKLAQLETLPDDELEPEFVQQVTEFCSYIFSHSMTKTLPGGIMVNGSRLKNLVLTYVN 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 HQKKLAQLETLPDDELEPEFVQQVTEFCSYIFSHSMTKTLPGGIMVNGSRLKNLVLTYVN 300

Qy        301 AISSGDLPCIENAVLALAQRENSAAVQKAIAHYDQQMGQKVQLPMETLQELLDLHRTSER 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 AISSGDLPCIENAVLALAQRENSAAVQKAIAHYDQQMGQKVQLPMETLQELLDLHRTSER 360

Qy        361 EAIEVFMKNSFKDVDQSFQKELETLLDAKQNDICKRNLEASSDYCSALLKDIFGPLEEAV 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 EAIEVFMKNSFKDVDQSFQKELETLLDAKQNDICKRNLEASSDYCSALLKDIFGPLEEAV 420

Qy        421 KQGIYSKPGGHNLFIQKTEELKAKYYREPRKGIQAEEVLQKYLKSKESVSHAILQTDQAL 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 KQGIYSKPGGHNLFIQKTEELKAKYYREPRKGIQAEEVLQKYLKSKESVSHAILQTDQAL 480

Qy        481 TETEKKKKEAQVKAEAEKAEAQRLAAIQRQNEQMMQERERLHQEQVRQMEIAKQNWLAEQ 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 TETEKKKKEAQVKAEAEKAEAQRLAAIQRQNEQMMQERERLHQEQVRQMEIAKQNWLAEQ 540

Qy        541 QKMQEQQMQ 549
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Db        541 QKMQEQQMQ 549


RESULT 2
Q86TM5
ID   Q86TM5      PRELIMINARY;      PRT;   489 AA.
AC   Q86TM5;
DT   01-JUN-2003 (TrEMBLrel. 24, Created)
DT   01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   CTCL tumor antigen GBP-5ta (Fragment).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Cutaneous lymphoma;
RX   PubMed=14996095;
RA   Hartmann T.B., Thiel D., Dummer R., Schadendorf D., Eichmuller S.;
RT   "SEREX identification of new tumour-associated antigens in cutaneous
RT   T-cell lymphoma.";
RL   Br. J. Dermatol. 150:252-258(2004).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Cutaneous lymphoma;
RX   PubMed=15175044;
RA   Fellenberg F., Hartmann T.B., Dummer R., Usener D., Schadendorf D.,
RA   Eichmuller S.;
RT   "GBP-5 splicing variants: New guanylate-binding proteins with tumor-
RT   associated expression and antigenicity.";
RL   J. Invest. Dermatol. 122:1510-1517(2004).
DR   EMBL; AF328727; AAO40731.1; -.
DR   HSSP; P32455; 1DG3.
DR   GO; GO:0005525; F:GTP binding; IEA.
DR   GO; GO:0003924; F:GTPase activity; IEA.
DR   GO; GO:0006955; P:immune response; IEA.
DR   InterPro; IPR003191; GBP.
DR   Pfam; PF02263; GBP; 1.
DR   Pfam; PF02841; GBP_C; 1.
FT   NON_TER     489    489
SQ   SEQUENCE   489 AA;  55247 MW;  B493C3586DFFDA1D CRC64;

  Query Match             82.7%;  Score 2516;  DB 2;  Length 489;
  Best Local Similarity   99.8%;  Pred. No. 1.8e-119;
  Matches  488;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MALEIHMSDPMCLIENFNEQLKVNQEALEILSAITQPVVVVAIVGLYRTGKSYLMNKLAG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MALEIHMSDPMCLIENFNEQLKVNQEALEILSAITQPVVVVAIVGLYRTGKSYLMNKLAG 60

Qy         61 KNKGFSVASTVQSHTKGIWIWCVPHPNWPNHTLVLLDTEGLGDVEKADNKNDIQIFALAL 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 KNKGFSVASTVQSHTKGIWIWCVPHPNWPNHTLVLLDTEGLGDVEKADNKNDIQIFALAL 120

Qy        121 LLSSTFVYNTVNKIDQGAIDLLHNVTELTDLLKARNSPDLDRVEDPADSASFFPDLVWTL 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 LLSSTFVYNTVNKIDQGAIDLLHNVTELTDLLKARNSPDLDRVEDPADSASFFPDLVWTL 180

Qy        181 RDFCLGLEIDGQLVTPDEYLENSLRPKQGSDQRVQNFNLPRLCIQKFFPKKKCFIFDLPA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 RDFCLGLEIDGQLVTPDEYLENSLRPKQGSDQRVQNFNLPRLCIQKFFPKKKCFIFDLPA 240
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Qy        241 HQKKLAQLETLPDDELEPEFVQQVTEFCSYIFSHSMTKTLPGGIMVNGSRLKNLVLTYVN 300
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Db        241 HQKKLAQLETLPDDELEPEFVQQVTEFCSYIFSHSMTKTLPGGIMVNGSRLKNLVLTYVN 300

Qy        301 AISSGDLPCIENAVLALAQRENSAAVQKAIAHYDQQMGQKVQLPMETLQELLDLHRTSER 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 AISSGDLPCIENAVLALAQRENSAAVQKAIAHYDQQMGQKVQLPMETLQELLDLHRTSER 360

Qy        361 EAIEVFMKNSFKDVDQSFQKELETLLDAKQNDICKRNLEASSDYCSALLKDIFGPLEEAV 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 EAIEVFMKNSFKDVDQSFQKELETLLDAKQNDICKRNLEASSDYCSALLKDIFGPLEEAV 420

Qy        421 KQGIYSKPGGHNLFIQKTEELKAKYYREPRKGIQAEEVLQKYLKSKESVSHAILQTDQAL 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 KQGIYSKPGGHNLFIQKTEELKAKYYREPRKGIQAEEVLQKYLKSKESVSHAILQTDQAL 480

Qy        481 TETEKKKKE 489
              ||||||||:
Db        481 TETEKKKKK 489


RESULT 3
Q8NF03
ID   Q8NF03      PRELIMINARY;      PRT;   504 AA.
AC   Q8NF03;
DT   01-OCT-2002 (TrEMBLrel. 22, Created)
DT   01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   FLJ00401 protein (Fragment).
GN   Name=FLJ00401;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Spleen;
RA   Jikuya H., Takano J., Kikuno R., Nagase T., Ohara O.;
RL   Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AK090479; BAC03460.1; -.
DR   HSSP; P32455; 1DG3.
DR   GO; GO:0005525; F:GTP binding; IEA.
DR   GO; GO:0003924; F:GTPase activity; IEA.
DR   GO; GO:0006955; P:immune response; IEA.
DR   InterPro; IPR003191; GBP.
DR   Pfam; PF02263; GBP; 1.
DR   Pfam; PF02841; GBP_C; 1.
FT   NON_TER       1      1
FT   NON_TER     504    504
SQ   SEQUENCE   504 AA;  56862 MW;  37E814E34539F743 CRC64;

  Query Match             81.8%;  Score 2490;  DB 2;  Length 504;
  Best Local Similarity   100.0%;  Pred. No. 3.9e-118;
  Matches  483;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MALEIHMSDPMCLIENFNEQLKVNQEALEILSAITQPVVVVAIVGLYRTGKSYLMNKLAG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         22 MALEIHMSDPMCLIENFNEQLKVNQEALEILSAITQPVVVVAIVGLYRTGKSYLMNKLAG 81

Qy         61 KNKGFSVASTVQSHTKGIWIWCVPHPNWPNHTLVLLDTEGLGDVEKADNKNDIQIFALAL 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         82 KNKGFSVASTVQSHTKGIWIWCVPHPNWPNHTLVLLDTEGLGDVEKADNKNDIQIFALAL 141

Qy        121 LLSSTFVYNTVNKIDQGAIDLLHNVTELTDLLKARNSPDLDRVEDPADSASFFPDLVWTL 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        142 LLSSTFVYNTVNKIDQGAIDLLHNVTELTDLLKARNSPDLDRVEDPADSASFFPDLVWTL 201

Qy        181 RDFCLGLEIDGQLVTPDEYLENSLRPKQGSDQRVQNFNLPRLCIQKFFPKKKCFIFDLPA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        202 RDFCLGLEIDGQLVTPDEYLENSLRPKQGSDQRVQNFNLPRLCIQKFFPKKKCFIFDLPA 261

Qy        241 HQKKLAQLETLPDDELEPEFVQQVTEFCSYIFSHSMTKTLPGGIMVNGSRLKNLVLTYVN 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        262 HQKKLAQLETLPDDELEPEFVQQVTEFCSYIFSHSMTKTLPGGIMVNGSRLKNLVLTYVN 321

Qy        301 AISSGDLPCIENAVLALAQRENSAAVQKAIAHYDQQMGQKVQLPMETLQELLDLHRTSER 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        322 AISSGDLPCIENAVLALAQRENSAAVQKAIAHYDQQMGQKVQLPMETLQELLDLHRTSER 381

Qy        361 EAIEVFMKNSFKDVDQSFQKELETLLDAKQNDICKRNLEASSDYCSALLKDIFGPLEEAV 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        382 EAIEVFMKNSFKDVDQSFQKELETLLDAKQNDICKRNLEASSDYCSALLKDIFGPLEEAV 441

Qy        421 KQGIYSKPGGHNLFIQKTEELKAKYYREPRKGIQAEEVLQKYLKSKESVSHAILQTDQAL 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        442 KQGIYSKPGGHNLFIQKTEELKAKYYREPRKGIQAEEVLQKYLKSKESVSHAILQTDQAL 501

Qy        481 TET 483
              |||
Db        502 TET 504


RESULT 4
Q8N4Q4
ID   Q8N4Q4      PRELIMINARY;      PRT;   481 AA.
AC   Q8N4Q4;
DT   01-OCT-2002 (TrEMBLrel. 22, Created)
DT   01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Similar to guanylate binding protein 5 (Fragment).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Ovary;
RA   Strausberg R.;
RL   Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC033761; AAH33761.1; -.
DR   HSSP; P32455; 1DG3.
DR   GO; GO:0005525; F:GTP binding; IEA.
DR   GO; GO:0003924; F:GTPase activity; IEA.
DR   GO; GO:0006955; P:immune response; IEA.
DR   InterPro; IPR003191; GBP.
DR   Pfam; PF02263; GBP; 1.
DR   Pfam; PF02841; GBP_C; 1.
FT   NON_TER       1      1
SQ   SEQUENCE   481 AA;  55070 MW;  3E642C58BCA06895 CRC64;

  Query Match             73.5%;  Score 2236;  DB 2;  Length 481;
  Best Local Similarity   99.8%;  Pred. No. 2.6e-105;
  Matches  439;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        110 KNDIQIFALALLLSSTFVYNTVNKIDQGAIDLLHNVTELTDLLKARNSPDLDRVEDPADS 169
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          5 KNDIQIFALALLLSSTFVYNTVNKIDQGAIDLLHNVTELTDLLKARNSPDLDRVEDPADS 64

Qy        170 ASFFPDLVWTLRDFCLGLEIDGQLVTPDEYLENSLRPKQGSDQRVQNFNLPRLCIQKFFP 229
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         65 ASFFPDLVWTLRDFCLGLEIDGQLVTPDEYLENSLRPKQGSDQRVQNFNLPRLCIQKFFP 124

Qy        230 KKKCFIFDLPAHQKKLAQLETLPDDELEPEFVQQVTEFCSYIFSHSMTKTLPGGIMVNGS 289
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        125 KKKCFIFDLPAHQKKLAQLETLPDDELEPEFVQQVTEFCSYIFSHSMTKTLPGGIMVNGS 184

Qy        290 RLKNLVLTYVNAISSGDLPCIENAVLALAQRENSAAVQKAIAHYDQQMGQKVQLPMETLQ 349
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        185 RLKNLVLTYVNAISSGDLPCIENAVLALAQRENSAAVQKAIAHYDQQMGQKVQLPMETLQ 244

Qy        350 ELLDLHRTSEREAIEVFMKNSFKDVDQSFQKELETLLDAKQNDICKRNLEASSDYCSALL 409
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        245 ELLDLHRTSEREAIEVFMKNSFKDVDQSFQKELETLLDAKQNDICKRNLEASSDYCSALL 304

Qy        410 KDIFGPLEEAVKQGIYSKPGGHNLFIQKTEELKAKYYREPRKGIQAEEVLQKYLKSKESV 469
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db        305 KDIFGPLEEAVKQGIYSKPGGHNLFIQKTEELKAKYYREPRKGIQAEEVLQKYLKSKESV 364

Qy        470 SHAILQTDQALTETEKKKKEAQVKAEAEKAEAQRLAAIQRQNEQMMQERERLHQEQVRQM 529
              ||||||||||||||:||||||||||||||||||||||||||||||||||||||||||||||
Db        365 SHAILQTDQALTETKKKKKEAQVKAEAEKAEAQRLAAIQRQNEQMMQERERLHQEQVRQM 424

Qy        530 EIAKQNWLAEQQKMQEQQMQ 549
              ||||||||||||||||||||
Db        425 EIAKQNWLAEQQKMQEQQMQ 444


RESULT 5
GBP1_HUMAN
ID   GBP1_HUMAN     STANDARD;      PRT;   592 AA.
AC   P32455;
DT   01-OCT-1993 (Rel. 27, Created)
DT   01-OCT-1993 (Rel. 27, Last sequence update)
DT   25-OCT-2004 (Rel. 45, Last annotation update)
DE   Interferon-induced guanylate-binding protein 1 (GTP-binding protein 1)
DE   (Guanine nucleotide-binding protein 1) (HuGBP-1).
GN   Name=GBP1;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=91342675; PubMed=1715024;
RA   Cheng Y.-S.E., Patterson C.E., Staeheli P.;
RT   "Interferon-induced guanylate-binding proteins lack an N(T)KXD
RT   consensus motif and bind GMP in addition to GDP and GTP.";
RL   Mol. Cell. Biol. 11:4717-4725(1991).
RN   [2]
RP   SEQUENCE FROM N.A.
RA   Kalnine N., Chen X., Rolfs A., Halleck A., Hines L., Eisenstein S.,
RA   Koundinya M., Raphael J., Moreira D., Kelley T., LaBaer J., Lin Y.,
RA   Phelan M., Farmer A.;
RT   "Cloning of human full-length CDSs in BD Creator(TM) system donor
RT   vector.";
RL   Submitted (MAY-2003) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Uterus;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [4]
RP   ISOPRENOID.
RX   MEDLINE=96427476; PubMed=8830800;
RA   Nantais D.E., Schwemmle M., Stickney J.T., Vestal D.J., Buss J.E.;
RT   "Prenylation of an interferon-gamma-induced GTP-binding protein: the
RT   human guanylate binding protein, huGBP1.";
RL   J. Leukoc. Biol. 60:423-431(1996).
RN   [5]
RP   X-RAY CRYSTALLOGRAPHY (1.8 ANGSTROMS).
RX   MEDLINE=20140138; PubMed=10676968; DOI=10.1038/35000617;
RA   Prakash B., Praefcke G.J.K., Renault L., Wittinghofer A., Herrmann C.;
RT   "Structure of human guanylate-binding protein 1 representing a unique
RT   class of GTP-binding proteins.";
RL   Nature 403:567-571(2000).
CC   -!- FUNCTION: Binds GTP, GDP and GMP.
CC   -!- INDUCTION: By interferon gamma during macrophage activation.
CC   -!- SIMILARITY: Belongs to the GBP family.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC   ---------------------------------------------------------------------
DR   EMBL; M55542; AAA35871.1; -.
DR   EMBL; BT006847; AAP35493.1; -.
DR   EMBL; BC002666; AAH02666.1; -.
DR   PIR; A41268; A41268.
DR   PDB; 1DG3; X-ray; A=1-592.
DR   PDB; 1F5N; X-ray; A=1-592.
DR   Genew; HGNC:4182; GBP1.
DR   H-InvDB; HIX0018119; -.
DR   MIM; 600411; -.
DR   GO; GO:0005525; F:GTP binding; TAS.
DR   InterPro; IPR003191; GBP.
DR   Pfam; PF02263; GBP; 1.
DR   Pfam; PF02841; GBP_C; 1.
KW   3D-structure; GTP-binding; Interferon induction; Lipoprotein;
KW   Multigene family; Polymorphism; Prenylation.
FT   NP_BIND      45    52       GTP.
FT   NP_BIND      97   101       GTP.
FT   LIPID       589   589       S-farnesyl cysteine.
FT   VARIANT     349   349       S -> T (in dbSNP:1048425).
FT                               /FTId=VAR_014849.
FT   STRAND       11    17
FT   TURN         18    19
FT   STRAND       20    23
FT   HELIX        25    32
FT   TURN         33    33
FT   STRAND       37    46
FT   TURN         47    48
FT   HELIX        51    58
FT   TURN         59    60
FT   STRAND       78    84
FT   TURN         89    90
FT   STRAND       92    98
FT   STRAND      101   101
FT   HELIX       104   106
FT   TURN        110   111
FT   HELIX       112   122
FT   STRAND      125   131
FT   HELIX       136   140
FT   TURN        141   142
FT   HELIX       143   146
FT   TURN        147   147
FT   HELIX       148   151
FT   STRAND      153   153
FT   HELIX       167   170
FT   HELIX       171   174
FT   STRAND      177   183
FT   TURN        184   184
FT   HELIX       198   205
FT   TURN        206   206
FT   HELIX       214   229
FT   STRAND      233   237
FT   HELIX       244   252
FT   HELIX       255   257
FT   HELIX       260   276
FT   STRAND      281   282
FT   TURN        283   285
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FT   STRAND      286    287
FT   STRAND      289    289
FT   HELIX       290    306
FT   TURN        307    307
FT   STRAND      311    311
FT   HELIX       312    342
FT   HELIX       350    371
FT   HELIX       376    378
FT   HELIX       379    423
FT   TURN        424    427
FT   TURN        430    431
FT   HELIX       432    449
FT   TURN        455    456
FT   HELIX       457    467
FT   TURN        468    468
FT   HELIX       469    478
FT   HELIX       484    563
FT   TURN        564    564
FT   HELIX       566    582
SQ   SEQUENCE   592 AA;  67902 MW;  FC05D1B0FB635467 CRC64;

  Query Match             64.4%;  Score 1958.5;  DB 1;  Length 592;
  Best Local Similarity   69.4%;  Pred. No. 3.6e-91;
  Matches  387;  Conservative   71;  Mismatches   89;  Indels   11;  Gaps    3;

Qy          1 MALEIHMSDPMCLIENFNEQLKVNQEALEILSAITQPVVVVAIVGLYRTGKSYLMNKLAG 60
              || ||||: ||||||| | :|  | |||:||||||||:||||||||||||||||||||||
Db          1 MASEIHMTGPMCLIENTNGRLMANPEALKILSAITQPMVVVAIVGLYRTGKSYLMNKLAG 60

Qy         61 KNKGFSVASTVQSHTKGIWIWCVPHPNWPNHTLVLLDTEGLGDVEKADNKNDIQIFALAL 120
              | ||||: ||||||||||||:||||||  | | |||||||||||||| ||:||  |||||:
Db         61 KKKGFSLGSTVQSHTKGIWMWCVPHPKKPGHILVLLDTEGLGDVEKGDNQNDSWIFALAV 120

Qy        121 LLSSTFVYNTVNKIDQGAIDLLHNVTELTDLLKARNSPD--LDRVEDPADSASFFPDLVW 178
              |||||||||::  |:| |:|  |: |||||  :::::|||   : ||| ||  ||||| ||
Db        121 LLSSTFVYNSIGTINQQAMDQLYYVTELTHRIRSKSSPDENENEVEDSADFVSFFPDFVW 180

Qy        179 TLRDFCLGLEIDGQLVTPDEYLENSLRPKQGSDQRVQNFNLPRLCIQKFFPKKKCFIFDL 238
              ||||| | || ||| :||||||  ||: |:|: |: : |||||||:|||||||||:||
Db        181 TLRDFSLDLEADGQPLTPDEYLTYSLKLKKGTSQKDETFNLPRLCIRKFFPKKKCFVFDR 240

Qy        239 PAHQKKLAQLETLPDDELEPEFVQQVTEFCSYIFSHSMTKTLPGGIMVNGSRLKNLVLTY 298
              | |::|||||| | |:||:|||||| :|||||||:| |||| ||| ||| ||::|||||
Db        241 PVHRRKLAQLEKLQDEELDPEFVQQVADFCSYIFSNSKTKTLSGGIQVNGPRLESLVLTY 300

Qy        299 VNAISSGDLPCIENAVLALAQRENSAAVQKAIAHYDQQMGQKVQLPMETLQELLDLHRTS 358
              ||||||||||:|||||||| ||||||||||||:|||||||| |:||||||| |
Db        301 VNAISSGDLPCMENAVLALAQIENSAAVQKAIAHYEQQMGQKVQLPTESLQELLDLHRDS 360

Qy        359 EREAIEVFMKNSFKDVDQSFQKELETLLDAKQNDICKRNLEASSDYCSALLKDIFGPLEE 418
              ||||||||:::|||||| |||||   |: |::| ||:| ||||| || ||: || ||||
Db        361 EREAIEVFIRSSFKDVDHLFQKELAAQLEKKRDDFCKQNQEASSDRCSGLLQVIFSPLEE 420

Qy        419 AVKQGIYSKPGGHNLFIQKTEELKAKYYREPRKGIQAEEVLQKYLKSKESVSHAILQTDQ 478
              || |||||||: ||:|| ::|| ||| ||||||||||:|| |||||||:: |||||||
Db        421 EVKAGIYSKPGGYRLFVQKLQDLKKKYYEEPRKGIQAEEILQTYLKSKESMTDAILQTDQ 480

Qy        479 ALTETEKKKKEAQVKAEAEKAEAQRLAAIQRQNEQMMQERERLHQEQVRQ----MEIAKQ 534
              ||| ||: :  :|||: :| |: |  :||:|||||:::|| :|| ::|    ||  :
Db        481 TLTEKEKEIEVERVKAESAQASAKMLQEMQRKNEQMMEQKERSYQEHLKQLTEKMENDRV 540

Qy        535 NWLAEQQ-----KMQEQQ 547
                | ||:     |:|||:
Db        541 QLLKEQERTLALKLQEQE 558


RESULT 6
Q8BMN7
ID   Q8BMN7      PRELIMINARY;      PRT;   724 AA.
AC   Q8BMN7;
DT   01-MAR-2003 (TrEMBLrel. 23, Created)
DT   01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Mus musculus adult male pituitary gland cDNA, RIKEN full-length
DE   enriched library, clone:5330409J06 product:weakly similar to GUANYLATE
DE   BINDING PROTEIN 5.
GN   Name=Gbp5;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Pituitary gland;
RX   MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA   Carninci P., Hayashizaki Y.;
RT   "High-efficiency full-length cDNA cloning.";
RL   Meth. Enzymol. 303:19-44(1999).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Pituitary gland;
RX   MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA   RIKEN FANTOM Consortium;
RT   "Functional annotation of a full-length mouse cDNA collection.";
RL   Nature 409:685-690(2001).
RN   [3]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Pituitary gland;
RA   The FANTOM Consortium,
RA   the RIKEN Genome Exploration Research Group Phase I & II Team;
RT   "Analysis of the mouse transcriptome based on functional annotation of
RT   60,770 full-length cDNAs.";
RL   Nature 420:563-573(2002).
RN   [4]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Pituitary gland;
RX   MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA   Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA   Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT   "Normalization and subtraction of cap-trapper-selected cDNAs to
RT   prepare full-length cDNA libraries for rapid discovery of new genes.";
RL   Genome Res. 10:1617-1630(2000).
RN   [5]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Pituitary gland;
RX   MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA   Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA   Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M.,
RA   Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA   Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA   Fujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA   Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
RA   Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT   "RIKEN integrated sequence analysis (RISA) system-384-format
RT   sequencing pipeline with 384 multicapillary sequencer.";
RL   Genome Res. 10:1757-1771(2000).
RN   [6]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Pituitary gland;
RA   Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
RA   Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
RA   Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
RA   Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
RA   Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
RA   Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
RA   Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
RA   Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
RA   Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
RA   Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
RA   Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
RL   Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AK030414; BAC26953.1; -.
DR   HSSP; P32455; 1DG3.
DR   MGD; MGI:2429943; Gbp5.
DR   GO; GO:0005525; F:GTP binding; IEA.
DR   GO; GO:0003924; F:GTPase activity; IEA.
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DR   GO; GO:0006955; P:immune response; IEA.
DR   InterPro; IPR003191; GBP.
DR   Pfam; PF02263; GBP; 1.
DR   Pfam; PF02841; GBP_C; 1.
SQ   SEQUENCE   724 AA;  80410 MW;  799C517B51DBF47C CRC64;

  Query Match           63.5%;  Score 1933;  DB 2;  Length 724;
  Best Local Similarity   64.9%;  Pred. No. 8.8e-90;
  Matches  392;  Conservative   70;  Mismatches  126;  Indels   16;  Gaps    5;

Qy          1 MALEIHMSDPMCLIENFNEQLKVNQEALEILSAITQPVVVVAIVGLYRTGKSYLMNKLAG 60
              || |||| :|:||| :    |  |||||:||||||||||||||||||||||||||||||
Db          1 MAPEIHMPEPLCLIGSTEGHLVTNQEALKILSAITQPVVVVAIVGLYRTGKSYLMNKLAG 60

Qy         61 KNKGFSVASTVQSHTKGIWIWCVPHPNWPNHTLVLLDTEGLGDVEKADNKNDIQIFALAL 120
              | ||||| ||||||||||:||||||  |:||||||||||||||| | ||| ||||||:
Db         61 KEKGFSVGSTVQSHTKGIWMWCVPHPQKPDHTLVLLDTEGLGDVEKDDKKNDTQIFALAI 120

Qy        121 LLSSTFVYNTVNKIDQGAIDLLHNVTELTDLLKARNSPDLDRV--EDPADSASFFPDLVW 178
              |||||||||:|||||||||||||||||||||: ||| | ::   | |||  ||||||||
Db        121 LLSSTFVYNTMNKIDQGAIDLLHNVTELTDLLRTRNSSDSNQTEGEGPAD-MSFFPDLVW 179

Qy        179 TLRDFCLGLEIDGQLVTPDEYLENSLRPKQGSDQRVQNFNLPRLCIQKFFPKKKCFIFDL 238
              ||||| | |: :|  :|  |||||||: |||||:| | ||||||||||||| ||||:||
Db        180 TLRDFFLDLQANGHAITSDEYLENSLKLKQGSDERTQTFNLPRLCIQKFFPVKKCFVFDA 239

Qy        239 PAHQKKLAQLETLPDDELEPEFVQQVTEFCSYIFSHSMTKTLPGGIMVNGSRLKNLVLTY 298
              ||   ||:|| || ::||  :||| ::||||:||: | |||||||| ||| ||::|||||
Db        240 PALGSKLSQLPTLSNEELNSDFVQDLSEFCSHIFTQSKTKTLPGGIQVNGPRLESLVLTY 299

Qy        299 VNAISSGDLPCIENAVLALAQRENSAAVQKAIAHYDQQMGQKVQLPMETLQELLDLHRTS 358
              |:||:|| || ||| |: ||:|||||||||| |||| | :||||| ||||||||||||
Db        300 VDAINSGALPSIENTVVTLARRENSAAVQKAIGHYDQLMSEKVQLPTETLQELLDLHRTC 359

Qy        359 EREAIEVFMKNSFKDVDQSFQKELETLLDAKQNDICKRNLEASSDYCSALLKDIFGPLEE 418
              ||||||:| |:|||| : |||||:|| |||::|||:| :||:  || ||  || |||:
Db        360 EREAIEIFRKHSFKDEGEFFQKELESLLSAKQDEICKKNADASAALCSTLLGSIFKPLEQ 419

Qy        419 AVKQGIYSKPGGHNLFIQKTEELKAKYYREPRKGIQAEEVLQKYLKSKESVSHAILQTDQ 478
              | |  | ||||| ||:|: |:||| | ::| || ||||||| || :||:|| ||||||
Db        420 EVAQEFYHKPGGHKLFLQRMEQLKANYRQQPGKGTQAEEVLQTYLNAKETVSRTILQTDQ 479

Qy        479 ALTETEKKKKEAQVKAEAEKAEAQRLAAIQRQNEQMMQERERLHQEQVRQMEIAKQNWLA 538
              ||: | : |  | :||| : ||||| ||: | ||   | || ||||:||: : |
Db        480 VLTDKEIQSKAEQERAEAARLEAQRLEAIRIQEEQRKAEMERQHQEQLRQIALEKARVAQ 539

Qy        539 EQQKMQEQQMQ---VFINCFISPL--------PVTMRVCSSGKEGEAARSCGSQQGVWSQ 587
              ||| : :|: |     | |      :: ::|  |:||  |  |:: |  |:
Db        540 EQQWILKQRAQGRCPVIWCLDLLLAEDEGPKQDLSQKLCCFGQEG--GRLSGAEDGAASE 597

Qy        588 KVWV 591
               :|:
Db        598 ALWI 601


RESULT 7
GBP5_MOUSE
ID   GBP5_MOUSE     STANDARD;      PRT;   590 AA.
AC   Q8CFB4; Q8CFA4;
DT   29-MAR-2004 (Rel. 43, Created)
DT   29-MAR-2004 (Rel. 43, Last sequence update)
DT   05-JUL-2004 (Rel. 44, Last annotation update)
DE   Interferon-induced guanylate-binding protein 5 (GTP-binding protein 5)
DE   (Guanine nucleotide-binding protein 5) (MuGBP-5).
GN   Name=Gbp5;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Swiss Webster;
RX   MEDLINE=22284156; PubMed=12396730; DOI=10.1089/107999002760274926;
RA   Nguyen T.T., Hu Y., Widney D.P., Mar R.C., Smith J.B.;
RT   "Murine GBP-5, a new member of the murine guanylate-binding protein
RT   family, is coordinately regulated with other GBPs in vivo and in
RT   vitro.";
RL   J. Interferon Cytokine Res. 22:899-909(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RA   Adams M., Mural R.;
RL   Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   SEQUENCE FROM N.A.
RC   STRAIN=NMRI; TISSUE=Breast tumor;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC   -!- SIMILARITY: Belongs to the GBP family.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; AF422243; AAN31451.1; -.
DR   EMBL; AY128412; AAN46362.1; -.
DR   EMBL; BC058555; AAH58555.1; -.
DR   HSSP; P32455; 1DG3.
DR   MGD; MGI:2429943; Gbp5.
DR   InterPro; IPR003191; GBP.
DR   Pfam; PF02263; GBP; 1.
DR   Pfam; PF02841; GBP_C; 1.
KW   GTP-binding; Lipoprotein; Multigene family; Prenylation.
FT   NP_BIND      45     52       GTP (By similarity).
FT   NP_BIND      97    101       GTP (By similarity).
FT   LIPID       587    587       S-geranylgeranyl cysteine (By
FT                                similarity).
FT   CONFLICT    488    490       KKA -> T (in Ref. 2).
FT   CONFLICT    501    501       K -> E (in Ref. 2).
SQ   SEQUENCE   590 AA;  66970 MW;  092C0B3F3E0E2D26 CRC64;

  Query Match           62.7%;  Score 1907.5;  DB 1;  Length 590;
  Best Local Similarity   68.5%;  Pred. No. 1.3e-88;
  Matches  379;  Conservative   62;  Mismatches  103;  Indels    9;  Gaps    3;

Qy          1 MALEIHMSDPMCLIENFNEQLKVNQEALEILSAITQPVVVVAIVGLYRTGKSYLMNKLAG 60
              || |||| :|:||| :    |  |||||:||||||||||||||||||||||||||||||
Db          1 MAPEIHMPEPLCLIGSTEGHLVTNQEALKILSAITQPVVVVAIVGLYRTGKSYLMNKLAG 60

Qy         61 KNKGFSVASTVQSHTKGIWIWCVPHPNWPNHTLVLLDTEGLGDVEKADNKNDIQIFALAL 120
              | ||||| ||||||||||:||||||  |:||||||||||||||| | ||| ||||||:
Db         61 KEKGFSVGSTVQSHTKGIWMWCVPHPQKPDHTLVLLDTEGLGDVEKDDKKNDTQIFALAI 120

Qy        121 LLSSTFVYNTVNKIDQGAIDLLHNVTELTDLLKARNSPDLDRV--EDPADSASFFPDLVW 178
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                 ||||||||||:||||||||||||||||||||||: ||| | ::   | |||  ||||||||
Db        121 LLSSTFVYNTMNKIDQGAIDLLHNVTELTDLLRTRNSSDSNQTEGEGPAD-MSFFPDLVW 179

Qy        179 TLRDFCLGLEIDGQLVTPDEYLENSLRPKQGSDQRVQNFNLPRLCIQKFFPKKKCFIFDL 238
                 ||||| | |: :|  :| |||||||: |||||:| | ||||||||||||| ||||:||
Db        180 TLRDFFLDLQANGHAITSDEYLENSLKLKQGSDERTQTFNLPRLCIQKFFPVKKCFVFDA 239

Qy        239 PAHQKKLAQLETLPDDELEPEFVQQVTEFCSYIFSHSMTKTLPGGIMVNGSRLKNLVLTY 298
                 ||   ||:|| || ::||  :||| ::||||:||: | ||||||||| ||| ||::|||||
Db        240 PALGSKLSQLPTLSNEELNSDFVQDLSEFCSHIFTQSKTKTLPGGIQVNGPRLESLVLTY 299

Qy        299 VNAISSGDLPCIENAVLALAQRENSAAVQKAIAHYDQQMGQKVQLPMETLQELLDLHRTS 358
                 |:||:|| || ||| |: ||:|||||||||||| |||| | :||||| ||||||||||||
Db        300 VDAINSGALPSIENTVVTLARRENSAAVQKAIGHYDQLMSEKVQLPTETLQELLDLHRTC 359

Qy        359 EREAIEVFMKNSFKDVDQSFQKELETLLDAKQNDICKRNLEASSDYCSALLKDIFGPLEE 418
                 ||||||:| |:|||| : |||||:|| |||::|||:| :||:  || ||  || |||:
Db        360 EREAIEIFRKHSFKDEGEFFQKELESLLSAKQDEICKKNADASAALCSTLLGSIFKPLEQ 419

Qy        419 AVKQGIYSKPGGHNLFIQKTEELKAKYYREPRKGIQAEEVLQKYLKSKESVSHAILQTDQ 478
                 | |  | ||||| ||:|: |:||| | ::| || ||||||| || :||:||  ||||||
Db        420 EVAQEFYHKPGGHKLFLQRMEQLKANYRQQPGKGTQAEEVLQTYLNAKETVSRTILQTDQ 479

Qy        479 ALTETEKKKKEAQVKAEAEKAEAQRLAAIQRQNEQMMQERERLHQEQVRQMEIAK----- 533
                 ||: | :||  | :||| : :|||| ||: | ||  | || ||||:||: : |
Db        480 VLTDKEIQKKAEQERAEAARLKAQRLEAIRIQEEQRKAEMERQHQEQLRQIALEKARVAQ 539

Qy        534 -QNWLAEQQKMQE 545
                | |: :|:  :|
Db        540 EQQWILKQRAQEE 552


RESULT 8
Q8BU78
ID   Q8BU78      PRELIMINARY;      PRT;   561 AA.
AC   Q8BU78;
DT   01-MAR-2003 (TrEMBLrel. 23, Created)
DT   01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Mus musculus 0 day neonate lung cDNA, RIKEN full-length enriched
DE   library, clone:E030025M22 product:weakly similar to GUANYLATE BINDING
DE   PROTEIN 5 (Fragment).
GN   Name=Gbp5;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Lung;
RX   MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA   Carninci P., Hayashizaki Y.;
RT   "High-efficiency full-length cDNA cloning.";
RL   Meth. Enzymol. 303:19-44(1999).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Lung;
RX   MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA   RIKEN FANTOM Consortium;
RT   "Functional annotation of a full-length mouse cDNA collection.";
RL   Nature 409:685-690(2001).
RN   [3]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Lung;
RA   The FANTOM Consortium,
RA   the RIKEN Genome Exploration Research Group Phase I & II Team;
RT   "Analysis of the mouse transcriptome based on functional annotation of
RT   60,770 full-length cDNAs.";
RL   Nature 420:563-573(2002).
RN   [4]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Lung;
RX   MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA   Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA   Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT   "Normalization and subtraction of cap-trapper-selected cDNAs to
RT   prepare full-length cDNA libraries for rapid discovery of new genes.";
RL   Genome Res. 10:1617-1630(2000).
RN   [5]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Lung;
RX   MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA   Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA   Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M.,
RA   Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA   Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA   Fujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA   Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
RA   Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT   "RIKEN integrated sequence analysis (RISA) system-384-format
RT   sequencing pipeline with 384 multicapillary sequencer.";
RL   Genome Res. 10:1757-1771(2000).
RN   [6]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Lung;
RA   Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
RA   Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
RA   Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
RA   Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
RA   Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
RA   Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
RA   Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
RA   Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
RA   Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
RA   Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
RA   Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
RL   Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AK087083; BAC39801.1; -.
DR   HSSP; P32455; 1DG3.
DR   MGD; MGI:2429943; Gbp5.
DR   GO; GO:0005525; F:GTP binding; IEA.
DR   GO; GO:0003924; F:GTPase activity; IEA.
DR   GO; GO:0006955; P:immune response; IEA.
DR   InterPro; IPR003191; GBP.
DR   Pfam; PF02263; GBP; 1.
DR   Pfam; PF02841; GBP_C; 1.
FT   NON_TER     561     561
SQ   SEQUENCE   561 AA;  63322 MW;  2C83B9838661FF39 CRC64;

  Query Match          62.6%;  Score 1905.5;  DB 2;  Length 561;
  Best Local Similarity   69.0%;  Pred. No. 1.6e-88;
  Matches  380;  Conservative   60;  Mismatches  108;  Indels    3;  Gaps    2;

Qy          1 MALEIHMSDPMCLIENFNEQLKVNQEALEILSAITQPVVVVAIVGLYRTGKSYLMNKLAG 60
                || |||| :|:||| :    |  |||||:||||||||||||||||||||||||||||
Db          1 MAPEIHMPEPLCLIGSTEGHLVTNQEALKILSAITQPVVVVAIVGLYRTGKSYLMNKLAG 60

Qy         61 KNKGFSVASTVQSHTKGIWIWCVPHPNWPNHTLVLLDTEGLGDVEKADNKNDIQIFALAL 120
                | ||||| ||||||||||:||||||  |:||||||||||||||| | ||| ||||||:
Db         61 KEKGFSVGSTVQSHTKGIWMWCVPHPQKPDHTLVLLDTEGLGDVEKDDKKNDTQIFALAI 120

Qy        121 LLSSTFVYNTVNKIDQGAIDLLHNVTELTDLLKARNSPDLDRV--EDPADSASFFPDLVW 178
                ||||||||||:|||||||||||||||||||: ||| | ::   | |||  ||||||||
Db        121 LLSSTFVYNTMNKIDQGAIDLLHNVTELTDLLRTRNSSDSNQTEGEGPAD-MSFFPDLVW 179

Qy        179 TLRDFCLGLEIDGQLVTPDEYLENSLRPKQGSDQRVQNFNLPRLCIQKFFPKKKCFIFDL 238
                 ||||| | |: :|  :| |||||||: |||||:| | ||||||||||||| ||||:||
Db        180 TLRDFFLDLQANGHAITSDEYLENSLKLKQGSDERTQTFNLPRLCIQKFFPVKKCFVFDA 239

Qy        239 PAHQKKLAQLETLPDDELEPEFVQQVTEFCSYIFSHSMTKTLPGGIMVNGSRLKNLVLTY 298
                 ||   ||:|| || ::||  :||| ::||||:||: | ||||||||| ||| ||::|||||
Db        240 PALGSKLSQLPTLSNEELNSDFVQDLSEFCSHIFTQSKTKTLPGGIQVNGPRLESLVLTY 299

Qy        299 VNAISSGDLPCIENAVLALAQRENSAAVQKAIAHYDQQMGQKVQLPMETLQELLDLHRTS 358
                 |:||:|| || ||| |: ||:|||||||||||| |||| | :||||| ||||||||||||
Db        300 VDAINSGALPSIENTVVTLARRENSAAVQKAIGHYDQLMSEKVQLPTETLQELLDLHRTC 359
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Qy        359 EREAIEVFMKNSFKDVDQSFQKELETLLDAKQNDICKRNLEASSDYCSALLKDIFGPLEE 418
              ||||||:| |:|||| : |||||||:|| |||::|||:| :||:  || ||  || |||:
Db        360 EREAIEIFRKHSFKDEGEFFQKELESLLSAKQDEICKKNADASAALCSTLLGSIFKPLEQ 419

Qy        419 AVKQGIYSKPGGHNLFIQKTEELKAKYYREPRKGIQAEEVLQKYLKSKESVSHAILQTDQ 478
              | |  | ||||| ||:|: |:||| | ::| || ||||||| || :||:||  ||||||
Db        420 EVAQEFYHKPGGHKLFLQRMEQLKANYRQQPGKGTQAEEVLQTYLNAKETVSRTILQTDQ 479

Qy        479 ALTETEKKKKEAQVKAEAEKAEAQRLAAIQRQNEQMMQERERLHQEQVRQMEIAKQNWLA 538
              ||: | : |  | :||| : ||||| ||: | ||   | || ||||:||: : |
Db        480 VLTDKEIQSKAEQERAEAARLEAQRLEAIRIQEEQRKAEMERQHQEQLRQIALEKARVAQ 539

Qy        539 EQQKMQEQQMQ 549
              ||| : :|: |
Db        540 EQQWILKQRAQ 550


RESULT 9
GBP2_HUMAN
ID   GBP2_HUMAN     STANDARD;      PRT;   591 AA.
AC   P32456; Q86TB0;
DT   01-OCT-1993 (Rel. 27, Created)
DT   01-NOV-1995 (Rel. 32, Last sequence update)
DT   05-JUL-2004 (Rel. 44, Last annotation update)
DE   Interferon-induced guanylate-binding protein 2 (GTP-binding protein 2)
DE   (Guanine nucleotide-binding protein 2) (HuGBP-2).
GN   Name=GBP2;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=91342675; PubMed=1715024;
RA   Cheng Y.-S.E., Patterson C.E., Staeheli P.;
RT   "Interferon-induced guanylate-binding proteins lack an N(T)KXD
RT   consensus motif and bind GMP in addition to GDP and GTP.";
RL   Mol. Cell. Biol. 11:4717-4725(1991).
RN   [2]
RP   REVISIONS.
RC   TISSUE=Foreskin;
RA   Schwemmle M.;
RL   Submitted (SEP-1991) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   SEQUENCE FROM N.A.
RA   Poustka A., Albert R., Moosmayer P., Schupp I., Wellenreuther R.,
RA   Mewes H.-W., Weil B., Amid C., Fobo G., Han M., Osanger A.,
RA   Wiemann S.;
RL   Submitted (APR-2003) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: Binds GTP, GDP and GMP.
CC   -!- INDUCTION: By interferon gamma during macrophage activation.
CC   -!- SIMILARITY: Belongs to the GBP family.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; M55543; AAA67323.1; -.
DR   EMBL; AL832451; CAD89925.1; -.
DR   PIR; S70524; S70524.
DR   HSSP; P32455; 1DG3.
DR   Genew; HGNC:4183; GBP2.
DR   H-InvDB; HIX0000764; -.
DR   MIM; 600412; -.
DR   GO; GO:0005525; F:GTP binding; TAS.
DR   GO; GO:0006955; P:immune response; TAS.
DR   InterPro; IPR003191; GBP.
DR   Pfam; PF02263; GBP; 1.
DR   Pfam; PF02841; GBP_C; 1.
KW   GTP-binding; Interferon induction; Lipoprotein; Multigene family;
KW   Prenylation.
FT   NP_BIND      45     52       GTP (By similarity).
FT   NP_BIND      97    101       GTP (By similarity).
FT   LIPID       588    588       S-geranylgeranyl cysteine (By
FT                                similarity).
FT   CONFLICT    303    303       S -> G (in Ref. 3).
SQ   SEQUENCE   591 AA;  67183 MW;  E090809EE18FC8A8 CRC64;

  Query Match             62.3%;  Score 1897;  DB 1;  Length 591;
  Best Local Similarity   63.5%;  Pred. No. 4.6e-88;
  Matches  377;  Conservative   88;  Mismatches  101;  Indels   28;  Gaps    4;

Qy          1 MALEIHMSDPMCLIENFNEQLKVNQEALEILSAITQPVVVVAIVGLYRTGKSYLMNKLAG 60
              || ||::  || ||:|   || || |||:|||||||||||||||||||||||||||||||
Db          1 MAPEINLPGPMSLIDNTKGQLVVNPEALKILSAITQPVVVVAIVGLYRTGKSYLMNKLAG 60

Qy         61 KNKGFSVASTVQSHTKGIWIWCVPHPNWPNHTLVLLDTEGLGDVEKADNKNDIQIFALAL 120
              |  |||: |||:|||||||:|||||  | ||||||||||||:|| ||:||  |||||:
Db         61 KKNGFSLGSTVKSHTKGIWMWCVPHPKKPEHTLVLLDTEGLGDIEKGDNENDSWIFALAI 120

Qy        121 LLSSTFVYNTVNKIDQGAIDLLHNVTELTDLLKARNSPDLDRVEDPADSASFFPDLVWTL 180
              |||||||||::  |:| |:| || |||||| :|| :||  : |:| ||  ||||  ||||
Db        121 LLSSTFVYNSMGTINQQAMDQLHYVTELTDRIKANSSPGNNSVDDSADFVSFFPAFVWTL 180

Qy        181 RDFCLGLEIDGQLVTPDEYLENSLRPKQGSDQRVQNFNLPRLCIQKFFPKKKCFIFDLPA 240
              ||| | ||:||: :| |:||| ||: ::|:|:: ::|| |||||:|||||:|||:|| ||
Db        181 RDFTLELEVDGEPITADDYLELSLKLRKGTDKKSKSFNDPRLCIRKFFPKRKCFVFDWPA 240

Qy        241 HQKKLAQLETLPDDELEPEFVQQVTEFCSYIFSHSMTKTLPGGIMVNGSRLKNLVLTYVN 300
              :| || || | ::|| |:|::|| |||||| ||| ||| ||| ||| ||::|||||||
Db        241 PKKYLAHLEQLKEEELNPDFIEQVAEFCSYILSHSNVKTLSGGIAVNGPRLESLVLTYVN 300

Qy        301 AISSGDLPCIENAVLALAQRENSAAVQKAIAHYDQQMGQKVQLPMETLQELLDLHRTSER 360
              |||||||||:|||||||| |||||:||||||:|||||||||| |||||||||| |||
Db        301 AISSGDLPCMENAVLALAQIENSAAVEKAIAHYEQQMGQKVQLPTETLQELLDLHRDSER 360

Qy        361 EAIEVFMKNSFKDVDQSFQKELETLLDAKQNDICKRNLEASSDYCSALLKDIFGPLEEAV 420
              |||||||||||||||| ||::|   |:|:::| ||:| :|||| | |||:||||||| |
Db        361 EAIEVFMKNSFKDVDQMFQRKLGAQLEARRDDFCKQNSKASSDCCMALLQDIFGPLEEDV 420

Qy        421 KQGIYSKPGGHNLFIQKTEELKAKYYREPRKGIQAEEVLQKYLKSKESVSHAILQTDQAL 480
              ||| :|||||: || || :||| ||||: |||||||:|||:|||:||| |: |:|||||:|
Db        421 KQGTFSKPGGYRLFTQKLQELKNKYYQVPRKGIQAKEVLKKYLESKEDVADALLQTDQSL 480

Qy        481 TETEKKKKEAQVKAEAEKAEAQRLAAIQRQNEQMMQERERLHQEQVRQ----MEIAKQNW 536
              :| ||  :  ::|||: :|  : |  ||::||:||:::|: :|| |:|    ||  :
Db        481 SEKEKAIEVERIKAESAEAAKKMLEEIQKKNEEMMEQKEKSYQEHVKQLTEKMERDRAQL 540

Qy        537 LAEQQ-----KMQEQQMQVFINCFISPLPVTMRVCSSGKEGEAARSCGSQQGVW 585
              :|||:     |:|||:                |:   | | |: |    |: :|
Db        541 MAEQEKTLALKLQEQE---------------RLLKEGFENESKR---LQKDIW 575


RESULT 10
Q6GPH0
ID   Q6GPH0      PRELIMINARY;      PRT;   591 AA.
AC   Q6GPH0;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Guanylate binding protein 2, interferon-inducible.
GN   Name=GBP2;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Skin;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
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RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Skin;
RA   Strausberg R.;
RL   Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC073163; AAH73163.1; -.
DR   GO; GO:0005525; F:GTP binding; IEA.
DR   GO; GO:0003924; F:GTPase activity; IEA.
DR   GO; GO:0006955; P:immune response; IEA.
DR   InterPro; IPR003191; GBP.
DR   Pfam; PF02263; GBP; 1.
DR   Pfam; PF02841; GBP_C; 1.
SQ   SEQUENCE   591 AA;  67233 MW;  739CE562AF335776 CRC64;

 Query Match             62.2%;  Score 1892;  DB 2;  Length 591;
 Best Local Similarity   63.5%;  Pred. No. 8.2e-88;
 Matches  377;  Conservative   87;  Mismatches  102;  Indels   28;  Gaps    4;

Qy          1 MALEIHMSDPMCLIENFNEQLKVNQEALEILSAITQPVVVVAIVGLYRTGKSYLMNKLAG 60
              || ||::  || ||:|   || || |||:||||||||||||||||||||||||||||||
Db          1 MAPEINLPGPMSLIDNTKGQLVVNPEALKILSAITQPVVVVAIVGLYRTGKSYLMNKLAG 60

Qy         61 KNKGFSVASTVQSHTKGIWIWCVPHPNWPNHTLVLLDTEGLGDVEKADNKNDIQIFALAL 120
              |  |||: |||:|||||||:|||||  | |||||||||||||:|| ||:||  |||||:
Db         61 KKNGFSLGSTVKSHTKGIWMWCVPHPKKPEHTLVLLDTEGLGDIEKGDNENDSWIFALAI 120

Qy        121 LLSSTFVYNTVNKIDQGAIDLLHNVTELTDLLKARNSPDLDRVEDPADSASFFPDLVWTL 180
              |||||||||::  |:| |:| || |||||| :|| :|| : |:| ||  ||||  ||||
Db        121 LLSSTFVYNSMGTINQQAMDQLHYVTELTDRIKANSSPGNNSVDDSADFVSFFPAFVWTL 180

Qy        181 RDFCLGLEIDGQLVTPDEYLENSLRPKQGSDQRVQNFNLPRLCIQKFFPKKKCFIFDLPA 240
              ||| | ||:||: :| |:||| ||: ::|:|:: ::|| ||||||:|||||:|||:|| ||
Db        181 RDFTLELEVDGEPITADDYLELSLKLRKGTDKKSKSFNDPRLCIRKFFPKRKCFVFDWPA 240

Qy        241 HQKKLAQLETLPDDELEPEFVQQVTEFCSYIFSHSMTKTLPGGIMVNGSRLKNLVLTYVN 300
              :| || || | ::|| |:|::|| |||||| ||| ||| ||| ||| ||::|||||||
Db        241 PKKYLAHLEQLKEEELNPDFIEQVAEFCSYILSHSNVKTLSGGIPVNGPRLESLVLTYVN 300

Qy        301 AISSGDLPCIENAVLALAQRENSAAVQKAIAHYDQQMGQKVQLPMETLQELLDLHRTSER 360
              ||||||||| |||||||:||||||:|||||||||| |||||||||| |||
Db        301 AISSGDLPCRENAVLALAQIENSAAVEKAIAHYEQQMGQKVQLPTETLQELLDLHRDSER 360

Qy        361 EAIEVFMKNSFKDVDQSFQKELETLLDAKQNDICKRNLEASSDYCSALLKDIFGPLEEAV 420
              |||||||||||||||| ||::|   |:|:::| ||:| :|||| | |||:||||||| |
Db        361 EAIEVFMKNSFKDVDQMFQRKLGAQLEARRDDFCKQNSKASSDCCMALLQDIFGPLEEDV 420

Qy        421 KQGIYSKPGGHNLFIQKTEELKAKYYREPRKGIQAEEVLQKYLKSKESVSHAILQTDQAL 480
              ||| :|||||: || || :||| |||: |||||||:|||:|||:||| |: |:|||||:|
Db        421 KQGTFSKPGGYRLFTQKLQELKNKYYQVPRKGIQAKEVLKKYLESKEDVADALLQTDQSL 480

Qy        481 TETEKKKKEAQVKAEAEKAEAQRLAAIQRQNEQMMQERERLHQEQVRQ----MEIAKQNW 536
              :| ||  :  ::|||: :|  : |  ||::||:||:::|: :|| |:|    ||  :
Db        481 SEKEKAIEVERIKAESAEAAKKMLEEIQKKNEEMMEQKEKSYQEHVKQLTEKMERDRAQL 540

Qy        537 LAEQQ-----KMQEQQMQVFINCFISPLPVTMRVCSSGKEGEAARSCGSQQGVW 585
              :|||:     |:|||:                 |:   | | |: |    |: :|
Db        541 MAEQEKTLALKLQEQE---------------RLLKEGFENESKR---LQKDIW 575


RESULT 11
Q9H0R5
ID   Q9H0R5      PRELIMINARY;      PRT;   563 AA.
AC   Q9H0R5;
DT   01-MAR-2001 (TrEMBLrel. 16, Created)
DT   01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Hypothetical protein DKFZp564C2478.
GN   Name=DKFZp564C2478;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Brain;
RG   The German cDNA Consortium;
RA   Ottenwaelder B., Obermaier B., Deutschenbaur S., Schaipp A.,
RA   Mewes H.W., Weil B., Amid C., Osanger A., Fobo G., Han M., Wiemann S.;
RL   Submitted (SEP-2004) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AL136680; CAB66615.1; -.
DR   HSSP; P32455; 1DG3.
DR   Genew; HGNC:4184; GBP3.
DR   GO; GO:0005525; F:GTP binding; IEA.
DR   GO; GO:0003924; F:GTPase activity; IEA.
DR   GO; GO:0006955; P:immune response; IEA.
DR   InterPro; IPR003191; GBP.
DR   Pfam; PF02263; GBP; 1.
DR   Pfam; PF02841; GBP_C; 1.
KW   Hypothetical protein.
SQ   SEQUENCE   563 AA;  64127 MW;  0C2FB7CE7FFCBCC3 CRC64;

  Query Match             58.3%;  Score 1774.5;  DB 2;  Length 563;
  Best Local Similarity   65.4%;  Pred. No. 6.8e-82;
  Matches  363;  Conservative   61;  Mismatches   90;  Indels   41;  Gaps    3;

Qy          1 MALEIHMSDPMCLIENFNEQLKVNQEALEILSAITQPVVVVAIVGLYRTGKSYLMNKLAG 60
              || ||||: ||||||| | :|  | |||:|||||||||||||||||||||||||||||
Db          1 MAPEIHMTGPMCLIENTNGELVANPEALKILSAITQPVVVVAIVGLYRTGKSYLMNKLAG 60

Qy         61 KNKGFSVASTVQSHTKGIWIWCVPHPNWPNHTLVLLDTEGLGDVEKADNKNDIQIFALAL 120
              ||||||: |||:|||||||:||||||  | |||||||||||||:| ||:||  || ||:
Db         61 KNKGFSLGSTVKSHTKGIWMWCVPHPKKPEHTLVLLDTEGLGDVKKGDNQNDSWIFTLAV 120

Qy        121 LLSSTFVYNTVNKIDQGAIDLLHNVTELTDLLKARNSPDLDRVEDPADSASFFPDLVWTL 180
              ||||| |||::  |:| |:| |: ||||||  :::::||| :  || ||  ||||| ||||
Db        121 LLSSTLVYNSMGTINQQAMDQLYYVTELTHRIRSKSSPDENENEDSADFVSFFPDFVWTL 180

Qy        181 RDFCLGLEIDGQLVTPDEYLENSLRPKQGSDQRVQNFNLPRLCIQKFFPKKKCFIFDLPA 240
              ||| | || ||| :|||||| ||:  ||:
Db        181 RDFSLDLEADGQPLTPDEYLEYSLKLTQGN---------------------------- 210

Qy        241 HQKKLAQLETLPDDELEPEFVQQVTEFCSYIFSHSMTKTLPGGIMVNGSRLKNLVLTYVN 300
              :|||||| | |:||:||||||| :|||||||:| |||| ||| |||  |::|||||:|
Db        211 --RKLAQLEKLQDEELDPEFVQQVADFCSYIFSNSKTKTLSGGIKVNGPCLESLVLTYIN 268

Qy        301 AISSGDLPCIENAVLALAQRENSAAVQKAIAHYDQQMGQKVQLPMETLQELLDLHRTSER 360
              ||| |||||:||||||||| ||||||||||||||||||||||| |||||||||| |||
Db        269 AISRGDLPCMENAVLALAQIENSAAVQKAIAHYDQQMGQKVQLPAETLQELLDLHRVSER 328

Qy        361 EAIEVFMKNSFKDVDQSFQKELETLLDAKQNDICKRNLEASSDYCSALLKDIFGPLEEAV 420
              || ||:|||||||| |||:|   || |::| ||:| ||||| ||||: || |||| |
Db        329 EATEVYMKNSFKDVDHLFQKKLAAQLDKKRDDFCKQNQEASSDRCSALLQVIFSPLEEEV 388

Qy        421 KQGIYSKPGGHNLFIQKTEELKAKYYREPRKGIQAEEVLQKYLKSKESVSHAILQTDQAL 480
              | |||||||: ||||| ::|: ||| ||||||||||:|| ||||||||: ||||||| |
Db        389 KAGIYSKPGGYCLFIQKLQDLEKKYYEEPRKGIQAEEILQTYLKSKESVTDAILQTDQIL 448
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Qy        481 TETEKKKKEAQVKAEAEKAEAQRLAAIQRQNEQMMQERERLHQEQVRQ----MEIAKQNW 536
              || ||: :   ||||: :| |: :  :| : :|||:|:|: :|| |:|    ||  :
Db        449 TEKEKEIEVECVKAESAQASAKMVEEMQIKYQQMMEEKEKSYQEHVKQLTEKMERERAQL 508

Qy        537 LAEQQ-----KMQEQ 546
              | ||:     |:|||
Db        509 LEEQEKTLTSKLQEQ 523


RESULT 12
GBP1_MOUSE
ID   GBP1_MOUSE     STANDARD;      PRT;   589 AA.
AC   Q01514;
DT   01-JUL-1993 (Rel. 26, Created)
DT   01-JUL-1993 (Rel. 26, Last sequence update)
DT   05-JUL-2004 (Rel. 44, Last annotation update)
DE   Interferon-induced guanylate-binding protein 1 (GTP-binding protein 1)
DE   (Guanine nucleotide-binding protein 1) (mGBP1) (mGBP-1) (Interferon-
DE   gamma inducible protein MAG-1).
GN   Name=Gbp1; Synonyms=Gbp-1, Mag-1, Mpa1;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=92091752; PubMed=1753106;
RA   Wynn T.A., Nicolet C.M., Paulnock D.M.;
RT   "Identification and characterization of a new gene family induced
RT   during macrophage activation.";
RL   J. Immunol. 147:4384-4392(1991).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=91342675; PubMed=1715024;
RA   Cheng Y.-S.E., Patterson C.E., Staeheli P.;
RT   "Interferon-induced guanylate-binding proteins lack an N(T)KXD
RT   consensus motif and bind GMP in addition to GDP and GTP.";
RL   Mol. Cell. Biol. 11:4717-4725(1991).
RN   [3]
RP   ISOPRENOID.
RX   MEDLINE=20346950; PubMed=10888661;
RA   Stickney J.T., Buss J.E.;
RT   "Murine guanylate-binding protein: incomplete geranylgeranyl
RT   isoprenoid modification of an interferon-gamma-inducible guanosine
RT   triphosphate-binding protein.";
RL   Mol. Biol. Cell 11:2191-2200(2000).
CC   -!- FUNCTION: Binds GTP, GDP and GMP.
CC   -!- INDUCTION: By interferon gamma during macrophage activation.
CC   -!- PTM: Prenylation of mouse GBP1 is incomplete. It persistently
CC       exists in the cell as a mixture of C20-modified and (more
CC       predominantly) nonmodified form.
CC   -!- SIMILARITY: Belongs to the GBP family.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; M63961; AAA39486.1; -.
DR   EMBL; M55544; AAA37666.1; -.
DR   PIR; A46459; A46459.
DR   HSSP; P32455; 1DG3.
DR   MGD; MGI:95666; Gbp1.
DR   InterPro; IPR003191; GBP.
DR   Pfam; PF02263; GBP; 1.
DR   Pfam; PF02841; GBP_C; 1.
KW   GTP-binding; Interferon induction; Lipoprotein; Multigene family;
KW   Prenylation.
FT   NP_BIND      45     52       GTP (By similarity).
FT   NP_BIND      97    101       GTP (By similarity).
FT   LIPID       586    586       S-geranylgeranyl cysteine (partial).
SQ   SEQUENCE   589 AA;  67711 MW;  1A2947DF443640CE CRC64;

  Query Match           58.0%;  Score 1765.5;  DB 1;  Length 589;
  Best Local Similarity  61.7%;  Pred. No. 2e-81;
  Matches  343;  Conservative   95;  Mismatches  109;  Indels    9;  Gaps    2;

Qy          1 MALEIHMSDPMCLIENFNEQLKVNQEALEILSAITQPVVVVAIVGLYRTGKSYLMNKLAG 60
              || |||||:|||||||    || :||||| |||||||||||||||||||||||||||||||
Db          1 MASEIHMSEPMCLIENTEAQLVINQEALRILSAITQPVVVVAIVGLYRTGKSYLMNKLAG 60

Qy         61 KNKGFSVASTVQSHTKGIWIWCVPHPNWPNHTLVLLDTEGLGDVEKADNKNDIQIFALAL 120
              |  |||: |||||||||||:||||||     |||||||||| |||| ||:||  |||||:
Db         61 KRTGFSLGSTVQSHTKGIWMWCVPHPKKAGQTLVLLDTEGLEDVEKGDNQNDCWIFALAV 120

Qy        121 LLSSTFVYNTVNKIDQGAIDLLHNVTELTDLLKARNSPDLDRVEDPADSASFFPDLVWTL 180
              ||||||:||::  |:| |:| || |||||||:|:::|||   |:: |:   |||  ||||
Db        121 LLSSTFIYNSIGTINQQAMDQLHYVTELTDLIKSKSSPDQSDVDNSANFVGFFPIFVWTL 180

Qy        181 RDFCLGLEIDGQLVTPDEYLENSLRPKQGSDQRVQNFNLPRLCIQKFFPKKKCFIFDLPA 240
              ||| | || ||: :|||||| ||  ::|:|:  : ||:|||||:|||||:|||||| |
Db        181 RDFSLDLEFDGESITPDEYLETSLALRKGTDENTKKFNMPRLCIRKFFPKRKCFIFDRPG 240

Qy        241 HQKKLAQLETLPDDELEPEFVQQVTEFCSYIFSHSMTKTLPGGIMVNGSRLKNLVLTYVN 300
              :|:|::|| : :|:|  |||:|| || |||||:|  ||| ||| ||| |||:|| |||:
Db        241 DRKQLSKLEWIQEDQLNKEFVEQVAEFTSYIFSYSGVKTLSGGITVNGPRLKSLVQTYVS 300

Qy        301 AISSGDLPCIENAVLALAQRENSAAVQKAIAHYDQQMGQKVQLPMETLQELLDLHRTSER 360
              || ||:|||:||||| ||| |||||||||| :|::|| ||: :| ||||||||||| ||
Db        301 AICSGELPCMENAVLTLAQIENSAAVQKAITYYEEQMNQKIHMPTETLQELLDLHRTCER 360

Qy        361 EAIEVFMKNSFKDVDQSFQKELETLLDAKQNDICKRNLEASSDYCSALLKDIFGPLEEAV 420
              |||||||||||||| ||:||   |:||::   |:|:: || :|| ||: :|  ||| |
Db        361 EAIEVFMKNSFKDVDQKFQEELGAQLEAKRDAFVKKNMDMSSAHCSDLLEGLFAHLEEEV 420

Qy        421 KQGIYSKPGGHNLFIQKTEELKAKYYREPRKGIQAEEVLQKYLKSKESVSHAILQTDQAL 480
              ||| : |||| ||:|: :||: || : | ||:||| :|:|| :||| ::  :|: ||:|
Db        421 KQGTFYKPGGYYLFLQRKQELEKKYIQTPGKGLQAEVMLRKYFESKEDLADTLLKMDQSL 480

Qy        481 TETEKKKKEAQVKAEAEKAEAQRLAAIQRQNEQMMQERERLHQEQVRQ----MEIAKQNW 536
              || ||: :  ::|||| :|  : || :|:::| :|:::|: :|| ::|    ||  ::
Db        481 TEKEKQIEMERIKAEAAEAANRALAEMQKKHEMLMEQKEQSYQEHMKQLTEKMEQERKEL 540

Qy        537 LAEQQ-----KMQEQQ 547
              :||||     |:|||:
Db        541 MAEQQRIISLKLQEQE 556


RESULT 13
Q8TCE5
ID   Q8TCE5       PRELIMINARY;      PRT;   481 AA.
AC   Q8TCE5;
DT   01-JUN-2002 (TrEMBLrel. 21, Created)
DT   01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   GBP2 protein.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Lung;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
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RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Lung;
RA   Strausberg R.;
RL   Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC022272; AAH22272.1; -.
DR   HSSP; P32455; 1DG3.
DR   GO; GO:0005525; F:GTP binding; IEA.
DR   GO; GO:0003924; F:GTPase activity; IEA.
DR   GO; GO:0006955; P:immune response; IEA.
DR   InterPro; IPR003191; GBP.
DR   Pfam; PF02263; GBP; 1.
DR   Pfam; PF02841; GBP_C; 1.
SQ   SEQUENCE   481 AA;  54034 MW;  2F8B66BEA92EED87 CRC64;

  Query Match           58.0%;  Score 1764;  DB 2;  Length 481;
  Best Local Similarity   71.1%;  Pred. No. 1.9e-81;
  Matches  342;  Conservative   64;  Mismatches   75;  Indels    0;  Gaps    0;

Qy          1 MALEIHMSDPMCLIENFNEQLKVNQEALEILSAITQPVVVVAIVGLYRTGKSYLMNKLAG 60
              || ||::  || ||:|   || || |||:||||||||||||||||||||||||||||||
Db          1 MAPEINLPGPMSLIDNTKGQLVVNPEALKILSAITQPVVVVAIVGLYRTGKSYLMNKLAG 60

Qy         61 KNKGFSVASTVQSHTKGIWIWCVPHPNWPNHTLVLLDTEGLGDVEKADNKNDIQIFALAL 120
              | .|||: |||:|||||||:|||||   | |||||||||||||:|| ||:||  |||||:
Db         61 KKNGFSLGSTVKSHTKGIWMWCVPHPKKPEHTLVLLDTEGLGDIEKGDNENDSWIFALAI 120

Qy        121 LLSSTFVYNTVNKIDQGAIDLLHNVTELTDLLKARNSPDLDRVEDPADSASFFPDLVWTL 180
              |||||||||::  |:| |:| || |||||| :|| :||  : |:| ||  ||||  ||||
Db        121 LLSSTFVYNSMGTINQQAMDQLHYVTELTDRIKANSSPGNNSVDDSADFVSFFPAFVWTL 180

Qy        181 RDFCLGLEIDGQLVTPDEYLENSLRPKQGSDQRVQNFNLPRLCIQKFFPKKKCFIFDLPA 240
              ||| | ||:||: :| |:||| ||: ::|:|:: ::|| |||||:|||||:|||:|| ||
Db        181 RDFTLELEVDGEPITADDYLELSLKLRKGTDKKSKSFNDPRLCIRKFFPKRKCFVFDWPA 240

Qy        241 HQKKLAQLETLPDDELEPEFVQQVTEFCSYIFSHSMTKTLPGGIMVNGSRLKNLVLTYVN 300
               :| || || | ::|| |:|::|| |||||| |||  ||| ||| ||| ||::|||||||
Db        241 PKKYLAHLEQLKEEELNPDFIEQVAEFCSYILSHSNVKTLSGGIPVNGPRLESLVLTYVN 300

Qy        301 AISSGDLPCIENAVLALAQRENSAAVQKAIAHYDQQMGQKVQLPMETLQELLDLHRTSER 360
              |||||||||:|||||||| |||||:||||||:|||||||||| |||||||||| |||
Db        301 AISSGDLPCMENAVLALAQIENSAAVEKAIAHYEQQMGQKVQLPTETLQELLDLHRDSER 360

Qy        361 EAIEVFMKNSFKDVDQSFQKELETLLDAKQNDICKRNLEASSDYCSALLKDIFGPLEEAV 420
              |||||||||||||||| ||::|   |:|:::| ||:| :|||| | |||:||||||||| |
Db        361 EAIEVFMKNSFKDVDQMFQRKLGAQLEARRDDFCKQNSKASSDCCMALLQDIFGPLEEDV 420

Qy        421 KQGIYSKPGGHNLFIQKTEELKAKYYREPRKGIQAEEVLQKYLKSKESVSHAILQTDQAL 480
              ||| :|||||: || || :||| |||: |||||||:|||:|||:||| |: |:|||||:|
Db        421 KQGTFSKPGGYRLFTQKLQELKNKYYQVPRKGIQAKEVLKKYLESKEDVADALLQTDQSL 480

Qy        481 T 481
              :
Db        481 S 481


RESULT 14
GBP2_RAT
ID   GBP2_RAT       STANDARD;      PRT;   589 AA.
AC   Q63663;
DT   29-MAR-2004 (Rel. 43, Created)
DT   29-MAR-2004 (Rel. 43, Last sequence update)
DT   05-JUL-2004 (Rel. 44, Last annotation update)
DE   Interferon-induced guanylate-binding protein 2 (GTP-binding protein 2)
DE   (Guanine nucleotide-binding protein 2) (p67).
GN   Name=Gbp2;
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A., TISSUE SPECIFICITY, AND ISOPRENOID.
RX   MEDLINE=94198287; PubMed=8148370; DOI=10.1016/0167-4781(94)90284-4;
RA   Asundi V.K., Stahl R.C., Showalter L., Conner K.J., Carey D.J.;
RT   "Molecular cloning and characterization of an isoprenylated 67 kDa
RT   protein.";
RL   Biochim. Biophys. Acta 1217:257-265(1994).
CC   -!- FUNCTION: Binds GTP, GDP and GMP (By similarity).
CC   -!- TISSUE SPECIFICITY: Ubiquitous.
CC   -!- INDUCTION: By interferon gamma.
CC   -!- SIMILARITY: Belongs to the GBP family.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; M80367; AAA19909.1; ALT_INIT.
DR   PIR; S43506; S43506.
DR   HSSP; P32455; 1DG3.
DR   InterPro; IPR003191; GBP.
DR   Pfam; PF02263; GBP; 1.
DR   Pfam; PF02841; GBP_C; 1.
KW   GTP-binding; Interferon induction; Lipoprotein; Multigene family;
KW   Prenylation.
FT   NP_BIND      45     52       GTP (By similarity).
FT   NP_BIND      97    101       GTP (By similarity).
FT   LIPID       586    586       S-geranylgeranyl cysteine.
SQ   SEQUENCE   589 AA;  67109 MW;  5E52B79102C2D97F CRC64;

  Query Match           57.8%;  Score 1757.5;  DB 1;  Length 589;
  Best Local Similarity   63.3%;  Pred. No. 5.2e-81;
  Matches  346;  Conservative   82;  Mismatches  116;  Indels    3;  Gaps    1;

Qy          1 MALEIHMSDPMCLIENFNEQLKVNQEALEILSAITQPVVVVAIVGLYRTGKSYLMNKLAG 60
              || ||||  |||||||    | :||||| ||||| ||||||||||||||||||||||||
Db          1 MASEIHMLQPMCLIENTEAHLVINQEALRILSAINQPVVVVAIVGLYRTGKSYLMNKLAG 60

Qy         61 KNKGFSVASTVQSHTKGIWIWCVPHPNWPNHTLVLLDTEGLGDVEKADNKNDIQIFALAL 120
              |  |||: |||||||||||:||||||      |||||||||||| ||:||  |||||:
Db         61 KRTGFSLGSTVQSHTKGIWMWCVPHPKKAGQTLVLLDTEGLGDVEKGDNQNDCWIFALAV 120

Qy        121 LLSSTFVYNTVNKIDQGAIDLLHNVTELTDLLKARNSPDLDRVEDPADSASFFPDLVWTL 180
              |||||||::  |:| |:| || |||||||:|:::|||   ::| |:   |||  || |
Db        121 LLSSTFVYNSMGTINQQAMDQLHYVTELTDLIKSKSSPDQSGIDDSANFVGFFPTFVWAL 180

Qy        181 RDFCLGLEIDGQLVTPDEYLENSLRPKQGSDQRVQNFNLPRLCIQKFFPKKKCFIFDLPA 240
              ||| | ||::|:|||||||||:||  |:|:|:: ::|| |||||:|||||| ||
Db        181 RDFSLELEVNGKLVTPDEYLEHSLTLKKGADKKTKSFNEPRLCIRKFFPKRKCFIFDRPA 240

Qy        241 HQKKLAQLETLPDDELEPEFVQQVTEFCSYIFSHSMTKTLPGGIMVNGSRLKNLVLTYVN 300
               :|:| :|||| ::||  |||:|| || |||||:|  ||| |||:||| |||:|| |||
Db        241 LRKQLCKLETLGEEELCSEFVEQVAEFTSYIFSYSAVKTLSGGIIVNGPRLKSLVQTYVG 300

Qy        301 AISSGDLPCIENAVLALAQRENSAAVQKAIAHYDQQMGQKVQLPMETLQELLDLHRTSER 360
              ||||| |||:|:||| ||| |||||||||| ||::|| ||:|:| ||||||||||  ||
Db        301 AISSGSLPCMESAVLTLAQIENSAAVQKAITHYEEQMNQKIQMPTETLQELLDLHRLIER 360

Qy        361 EAIEVFMKNSFKDVDQSFQKELETLLDAKQNDICKRNLEASSDYCSALLKDIFGPLEEAV 420
              ||||:|:|||||||||| || ||  || :|::   |:| : || :|| |::|||||||| |
Db        361 EAIEIFLKNSFKDVDQKFQTELGNLLISKRDAFIKKNSDVSSAHCSDLIEDIFGPLEEEV 420
```

```
Qy        421 KQGIYSKPGGHNLFIQKTEELKAKYYREPRKGIQAEEVLQKYLKSKESVSHAILQTDQAL 480
              ||| :|||||: ||:|  :||: || : | ||::|| ||:|| :||| :   :|:|||:|
Db        421 KQGTFSKPGGYFLFLQMRQELEKKYNQAPGKGLEAEAVLKKYFESKEDIVETLLKTDQSL 480

Qy        481 TETEKKKKEAQVKAEAEKAEAQRLAAIQRQNEQMMQERERLHQEQVRQMEIAKQNWLAEQ 540
              ||  |: :  ::|||  :|  : ||  | : | |||::|  :|| |||:    :    ||
Db        481 TEAAKEIEVERIKAETAEAANRELAEKQEKFELMMQQKEESYQEHVRQL---TEKMKEEQ 537

Qy        541 QKMQEQQ 547
              :|: |:|
Db        538 KKLIEEQ 544


RESULT 15
GBP2_MOUSE
ID   GBP2_MOUSE     STANDARD;      PRT;   589 AA.
AC   Q9Z0E6; Q8CIC6; Q921N2; Q9R1I0;
DT   29-MAR-2004 (Rel. 43, Created)
DT   29-MAR-2004 (Rel. 43, Last sequence update)
DT   05-JUL-2004 (Rel. 44, Last annotation update)
DE   Interferon-induced guanylate-binding protein 2 (GTP-binding protein 2)
DE   (Guanine nucleotide-binding protein 2) (mGBP2) (mGBP-2).
GN   Name=Gbp2;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6;
RX   MEDLINE=99077537; PubMed=9862701;
RA   Boehm U., Guethlein L., Klamp T., Ozbek K., Schaub A., Fuetterer A.,
RA   Pfeffer K., Howard J.C.;
RT   "Two families of GTPases dominate the complex cellular response to
RT   IFN-gamma.";
RL   J. Immunol. 161:6715-6723(1998).
RN   [2]
RP   SEQUENCE FROM N.A., AND ISOPRENOID.
RC   STRAIN=C57BL/6; TISSUE=Bone marrow;
RX   MEDLINE=99074031; PubMed=9858320;
RA   Vestal D.J., Buss J.E., McKercher S.R., Jenkins N.A., Copeland N.G.,
RA   Kelner G.S., Asundi V.K., Maki R.A.;
RT   "Murine GBP-2: a new IFN-gamma-induced member of the GBP family of
RT   GTPases isolated from macrophages.";
RL   J. Interferon Cytokine Res. 18:977-985(1998).
RN   [3]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6; TISSUE=Kidney;
RX   MEDLINE=99313432; PubMed=10386861; DOI=10.1089/107999099313938;
RA   Anderson S.L., Carton J.M., Zhang X., Rubin B.Y.;
RT   "Genomic organization and chromosomal localization of a new member of
RT   the murine interferon-induced guanylate-binding protein family.";
RL   J. Interferon Cytokine Res. 19:487-494(1999).
RN   [4]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Mammary gland;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC   -!- FUNCTION: Binds GTP, GDP and GMP (By similarity).
CC   -!- INDUCTION: By interferon gamma during macrophage activation.
CC   -!- SIMILARITY: Belongs to the GBP family.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; AJ007970; CAA07797.1; -.
DR   EMBL; AF077007; AAC98287.1; -.
DR   EMBL; AF109168; AAD39746.1; -.
DR   EMBL; BC011336; AAH11336.1; -.
DR   EMBL; BC032882; AAH32882.1; -.
DR   HSSP; P32455; 1DG3.
DR   MGD; MGI:102772; Gbp2.
DR   InterPro; IPR003191; GBP.
DR   Pfam; PF02263; GBP; 1.
DR   Pfam; PF02841; GBP_C; 1.
KW   GTP-binding; Interferon induction; Lipoprotein; Multigene family;
KW   Prenylation.
FT   NP_BIND      45     52       GTP (By similarity).
FT   NP_BIND      97    101       GTP (By similarity).
FT   LIPID       586    586       S-geranylgeranyl cysteine.
FT   CONFLICT    163    163       V -> I (in Ref. 4).
FT   CONFLICT    246    246       S -> T (in Ref. 3).
FT   CONFLICT    381    381       E -> D (in Ref. 4; AAH11336).
SQ   SEQUENCE   589 AA;  66739 MW;  8E68B0A3BC5F3AE3 CRC64;

  Query Match             57.5%;  Score 1750.5;  DB 1;  Length 589;
  Best Local Similarity   62.8%;  Pred. No. 1.2e-80;
  Matches  349;  Conservative   84;  Mismatches  114;  Indels    9;  Gaps    2;

Qy          1 MALEIHMSDPMCLIENFNEQLKVNQEALEILSAITQPVVVVAIVGLYRTGKSYLMNKLAG 60
              || |||||:|||||||   || :||||| |||||||||||||||||||||||||||||||
Db          1 MASEIHMSEPMCLIENTEAQLVINQEALRILSAITQPVVVVAIVGLYRTGKSYLMNKLAG 60

Qy         61 KNKGFSVASTVQSHTKGIWIWCVPHPNWPNHTLVLLDTEGLGDVEKADNKNDIQIFALAL 120
              |  |||: |||||||||||:||||||      |||||||||| |||| ||:||  |||||:
Db         61 KRTGFSLGSTVQSHTKGIWMWCVPHPKKAGQTLVLLDTEGLEDVEKGDNQNDCWIFALAV 120

Qy        121 LLSSTFVYNTVNKIDQGAIDLLHNVTELTDLLKARNSPDLDRVEDPADSASFFPDLVWTL 180
              ||||||:||::  |:| |:| || |||||||:|:::|||   |:| |:   |||  ||||
Db        121 LLSSTFIYNSIGTINQQAMDQLHYVTELTDLIKSKSSPDQSGVDDSANFVGFFPTFVWTL 180

Qy        181 RDFCLGLEIDGQLVTPDEYLENSLRPKQGSDQRVQNFNLPRLCIQKFFPKKKCFIFDLPA 240
              ||| | ||::|: || |||||:||  |:|:|:: ::|| |||||:|||||:|||||| ||
Db        181 RDFSLELEVNGKPVTSDEYLEHSLTLKKGADKKTKSFNEPRLCIRKFFPKRKCFIFDRPA 240

Qy        241 HQKKLAQLETLPDDELEPEFVQQVTEFCSYIFSHSMTKTLPGGIMVNGSRLKNLVLTYVN 300
              :|:|::|||| ::||  |||:|| || ||| |:|  ||| |||:||| |||:|| |||
Db        241 QRKQLSKLETLREEELCGEFVEQVAEFTSYILSYSSVKTLCGGIIVNGPRLKSLVQTYVG 300

Qy        301 AISSGDLPCIENAVLALAQRENSAAVQKAIAHYDQQMGQKVQLPMETLQELLDLHRTSER 360
              |||:| |||:|:||| ||| |||||||||| ||::|| ||:|:| ||||||||||  |
Db        301 AISNGSLPCMESAVLTLAQIENSAAVQKAITHYEEQMNQKIQMPTETLQELLDLHRPIES 360

Qy        361 EAIEVFMKNSFKDVDQSFQKELETLLDAKQNDICKRNLEASSDYCSALLKDIFGPLEEAV 420
              ||||||:|||||||| || ||  || ||::   |:|:: ||  || ||:|||||||| |
Db        361 EAIEVFLKNSFKDVDQKFQTELGNLLVAKRDAFIKKNMDVSSARCSDLLEDIFGPLEEEV 420

Qy        421 KQGIYSKPGGHNLFIQKTEELKAKYYREPRKGIQAEEVLQKYLKSKESVSHAILQTDQAL 480
              | | :|||||: ||:|  :||: || : | ||:||| :|: |  ||  |   :|||||:|
Db        421 KLGTFSKPGGYYLFLQMRQELEKKYNQAPGKGLQAEAMLKNYFDSKADVVETLLQTDQSL 480

Qy        481 TETEKKKKEAQVKAEAEKAEAQRLAAIQRQNEQMMQERERLHQEQVR----QMEIAKQNW 536
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                ||  |: :| : |||| :|  : |   |:: | |||::|: :|| |:    :|:  ::
Db        481 TEAAKEVEEERTKAEAAEAANRELEKKQKEFELMMQQKEKSYQEHVKKLTEKMKDEQKQL 540

Qy        537 LAEQQ-----KMQEQQ 547
                ||||:     |::||:
Db        541 LAEQENIIAAKLREQE 556
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Search completed: July 9, 2005, 13:28:45
Job time : 175 secs